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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:24 ; Search time 28.88 Seconds
(without alignments)
117.402 Million cell updates/sec

Title: US-09-508-095-14

Perfect score: 65

Sequence: 1 ABRARVWCavg 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1566107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_290a04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed;
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	12	2 AAW93878	Aaw93878 Bifidobac
2	65	100.0	13	2 AAW93880	Aaw93880 Bifidobac
3	65	100.0	687	2 AAW71183	Aaw71183 Mutant hu
4	65	100.0	687	4 AAG77911	Aag77911 Human lac
5	65	100.0	688	2 AAW71182	Aaw71182 Mutant hu
6	65	100.0	688	4 AAG77910	Aag77910 Human lac
7	65	100.0	689	2 AAW71181	Aaw71181 Mutant hu
8	65	100.0	689	4 AAG77909	Aag77909 Human lac
9	65	100.0	690	2 AAW71180	Aaw71180 Mutant hu
10	65	100.0	690	4 AAG77908	Aag77908 Human lac
11	65	100.0	690	5 ABG80724	Abg80724 Codon opt
12	65	100.0	690	5 AAG77884	Aag77884 Human cod
13	65	100.0	692	2 AAY58733	Aay58733 Human lac
14	65	100.0	692	4 AAB97382	Aab97382 Human lac
15	65	100.0	692	4 AAG77906	Aag77906 Human lac
16	65	100.0	692	5 AAE28002	Aae28002 Human cod
17	65	100.0	693	2 AAR51146	Aar51146 Lactoferr
18	65	100.0	705	2 AAR22423	Aar22423 Human lac
19	65	100.0	705	2 AAY31152	Aay31152 Human lac
20	65	100.0	708	2 AAR22424	Aar22424 Human lac
21	65	100.0	708	2 AAY31153	Aay31153 Human lac
22	65	100.0	709	2 AAR12583	Aar12583 Lactoferr
23	65	100.0	709	2 AAR45198	Aar45198 Human lac
24	65	100.0	709	2 AAR45199	Aar45199 Human lac
25	65	100.0	709	2 AAW21695	Aaw21695 Human lac

26	65	100.0	709	2 AAW53879	Aaw53879 Human lac
27	65	100.0	709	3 AAY77577	Aay77577 Human lac
28	65	100.0	709	3 AAB03830	Aab03830 Human lac
29	65	100.0	709	4 AAB36842	Aab36842 Protein e
30	65	100.0	709	7 ADE76659	Ade76659 Human lac
31	65	100.0	711	2 AAR08033	Aar08033 Human lac
32	65	100.0	711	2 AAR43653	Aar43653 Lactoferr
33	65	100.0	711	2 AAW09342	Aaw09342 Human lac
34	65	100.0	711	2 AAW57317	Aaw57317 Human lac
35	65	100.0	711	2 AAW53880	Aaw53880 Bovine al
36	65	100.0	711	2 AAW68021	Aaw68021 Human lac
37	65	100.0	711	3 AAY77578	Aay77578 Human lac
38	65	100.0	711	3 AAB03831	Aab03831 Human lac
39	65	100.0	711	3 AAB08182	Aab08182 Amino aci
40	65	100.0	711	4 AAB36843	Aab36843 Human lac
41	65	100.0	711	4 AAE02341	Aae02341 Human lac
42	65	100.0	711	4 AAG64828	Aag64828 Chronic h
43	65	100.0	711	7 ADE76661	Ade76661 Human lac
44	58	89.2	685	2 AAR11664	Aar11664 Partial p
45	58	89.2	685	2 AAR11663	Aar11663 Partial p

ALIGNMENTS

RESULT 1
AAW93878 standard; peptide: 12 AA.
ID AAW93878
AAW93878;
27-AUG-2003 (revised)
DT 25-JUN-1999 (first entry)
XX
DE Bifidobacterium bifidus stimulating peptide 14.
XX Bifidogenic peptide; protease; treatment; microbe-related disease;
XX bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmidia;
KW infection; inflammation; microbial induced tumour; degenerative disorder;
KW diarrhoea; colici; oral microflora; intestinal microflora; caries;
KW vaginal microflora.
XX
OS Bifidobacterium bifidum.
XX
PN WO9914231-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WC-EP005899.
XX
PR 16-SEP-1997; 97DE-01040604.
XX
PR 11-FEB-1998; 98DE-01005385.
XX
PA (FORSS/) FORSSMANN W.
XX
PI Forssmann W, Zucht H, Liepke C;
XX
DR WPI; 1999-244022/20.
XX
PT Milk-derived peptides that stimulate Bifidobacterium bifidus.
XX
PS Claim 2; Page 3; 25pp; German.
XX
CC This invention describes milk-derived bifidogenic peptides and their
CC active derivatives or fragments, and combinations of them produced by
CC chemical coupling. Such are produced from bovine or human milk by
CC treatment for 2 hr with proteases, then centrifuging to remove fat and
CC acidifying to pH 2 to precipitate proteins. The solution phase is then
CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
CC Bifidobacterium bifidus and Escherichia coli in presence of the
CC fractions. Those fractions for which (BW-B0) -(EW-E0) is at least 0.15 are

CC selected where Bw = germ count after 16 hr culture of *B. bifidus* in 50%
 CC Elikker broth containing peptide at 0.2 mg/ml, B0 = germ count under 16 hr
 CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of *E. coli* in 3 g/l tryptic broth containing peptide at 0.2
 CC mg/ml, B0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W9388 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or caries. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX
 SQ Sequence 12 AA;

QY Query Match 100.0%; Score 65; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ARRRRVWCavg 12
 1 ARRRRVWCavg 12

RESULT 2
 AAW93880
 ID AAW93880 standard; peptide; 13 AA.
 XX
 AC AAW93880;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-JUN-1999 (first entry)
 XX
 DE Bifidobacterium bifidus stimulating peptide 16.
 XX
 KM Bifidogenic peptide; protease; treatment; microbe-related disease;
 KM bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
 KM infection; inflammation; microbial induced tumour; degenerative disorder;
 KM diarrhoea; colic; oral microflora; intestinal microflora; caries;
 KM vaginal microflora.
 KM
 XX
 OS Bifidobacterium bifidum.
 XX
 PN WO9914231-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-EP005899.
 XX
 PR 16-SEP-1997; 97DE-01040604.
 PR 11-FEB-1998; 98DE-01005385.
 XX
 PA (FORS/) FORSSMANN W.
 XX
 PI Forsemann W, Zucht H, Liepke C;
 XX
 DR WPI; 1999-244022/20.
 XX
 PT Milk-derived peptides that stimulate Bifidobacterium bifidus.
 XX
 PS Claim 2; Page 3; 25pp; German.
 XX
 CC This invention describes milk-derived bifidogenic peptides and their
 CC active derivatives or fragments, and combinations of them produced by
 CC chemical coupling. Such are produced from bovine or human milk by
 CC treatment for 2 hr with proteases, then centrifuging to remove fat and
 CC acidifying to pH 2 to precipitate proteins. The solution phase is then
 CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
 CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
 CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
 CC Bifidobacterium bifidus and *Escherichia coli* in presence of the
 CC fractions. Those fractions for which (Bw-B0)-(Bw-E0) is at least 0.15 are
 CC selected where Bw = germ count after 16 hr culture of *B. bifidus* in 50%
 CC Elikker broth containing peptide at 0.2 mg/ml, B0 = germ count under

CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of *E. coli* in 3 g/l tryptic broth containing peptide at 0.2
 CC mg/ml, B0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W9388 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or caries. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX
 SQ Sequence 13 AA;

QY Query Match 100.0%; Score 65; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ARRRRVWCavg 12
 1 ARRRRVWCavg 12

RESULT 3
 AAW71183
 ID AAW71183 standard; protein; 687 AA.
 XX
 AC AAW71183;
 XX
 DT 27-OCT-1998 (first entry)
 DT
 XX
 DE Mutant human lactoferrin protein designated hLF-5N.
 XX
 KM Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
 KM anti-infective; coagulant; complement activation; inhibition;
 KM LPS mediated activation; myeloperoxidase; growth promotion;
 KM intestinal epithelial cell; hydroxyl-radical formation;
 KM intestinal iron uptake; excretion.
 KM
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9833509-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98WO-IB000441.
 XX
 PR 03-FEB-1997; 97US-0036859P.
 PR 02-FEB-1998; 98US-00017043.
 XX
 PA (PHAR-) PHARMING BV.
 XX
 PI Nuijens J, Van Berckel PHC;
 XX
 DR WPI; 1998-437164/37.
 XX
 PT Compositions containing human lactoferrin and variants - are used for
 PT treating e.g. anaemia, iron-storage disease, inflammation, tumours,
 PT rheumatoid arthritis, ulcerative colitis or infections.
 XX
 PS Claim 2; Page; 70pp; English.
 XX
 CC AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
 CC The lactoferrin variants bind heparin with lower affinity than natural
 CC lactoferrin. The lactoferrin variants exhibit biological activities such
 CC as anti-inflammatory, anti-viral and anti-infective activities as well as
 CC a pro- and anti-coagulant effects, modulation of complement activation,
 CC inhibition of LPS mediated activation of neutrophils, inhibition of
 CC myeloperoxidase, regulation of transcription, growth promotion of intestinal
 CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
 CC intestinal iron uptake and excretion. note: This sequence does not appear
 CC in the specification; it was created using information provided

XX
 SO Sequence 687 AA;

Query Match	100.0%	Score 65	DB 2	Length 687
Best Local Similarity	100.0%	Pred. No. 0.0046		
Matches 12	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ARRARVWCavg 12		
DB	336	ARRARVWCavg 347		
RESULT 4				
AA677911	AA677911	standard; protein; 687 AA.		
XX	AA677911			
XX	22-JAN-2002	(first entry)		
XX	Human lactoferrin variant hLF-5N.			
XX	Human; lactoferrin; hLF; infectious disease; inflammatory disease;			
XX	excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;			
XX	anaemia; myelopoiesis; reperfusion injury; cytokine release; proteoglycan;			
XX	hLF-5N; mutant; muten.			
OS	Homo sapiens.			
XX	Key	Location/Qualifiers		
FT	Domain	23..26		
FT		/label= Cationic_domain		
XX	MO200172322-A2.			
PN	04-OCT-2001.			
PD	27-MAR-2001; 2001WO-NL000253.			
PF	27-MAR-2000; 2000EP-00201110.			
XX	27-MAR-2000; 2000US-0193352P.			
PR	(PHAR-) PHARMING INTELLECTUAL PROPERTY BV.			
PA	Van Bree JBM, Nuijens JH;			
P1	WPI; 2001-648424/74.			
DR	Use of lactoferrin for treatment of infectious diseases, inflammatory			
PT	diseases and excess of heparin.			
PT	Claim 10; Page; 49pp; English.			
PS	The sequence represents the human lactoferrin (hLF) protein variant hLF-			
XX	5N. The invention relates to novel methods of treatment using high doses			
XX	of lactoferrin. The methods of the invention are useful for the treatment			
CC	or prophylaxis of infectious diseases, inflammatory diseases and excess			
CC	of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,			
CC	anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and			
CC	proteoglycan-mediated entry of virus into cells. The advantage of the			
CC	method is that the patient is substantially free of side effect responses			
CC	to administration of lactoferrin. Therefore large doses of lactoferrin			
CC	can be administered. Note: The present sequence is not shown in the			
CC	specification but is derived from human wild-type lactoferrin sequence			
CC	given in the sequence listing of the specification			
XX	Sequence 687 AA;			
SO	Query Match	100.0%; Score 65; DB 4; Length 687;		
	Best Local Similarity	100.0%; Pred. No. 0.0046;		
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	1	ARRARVWCavg 12		
DB	336	ARRARVWCavg 347		

[illegible]

XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
KW anaemia; myelopolesis; reperfusion injury; cytokine release; proteoglycan;
KW hLF-4N; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 24..27
FT /label= Cationic_domain
XX
PN WO200172322-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-NL000253.
XX
PR 27-MAR-2000; 2000EP-00201110.
PR 27-MAR-2000; 2000US-0193352P.
XX
PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX
PI Van Bree JBM, Nuijens JH;
XX
DR WPI: 2001-648424/74.
XX
PT Use of lactoferrin for treatment of infectious diseases, inflammatory
PS diseases and excess of heparin.
XX
PS Claim 10; Page: 49pp; English.
XX
CC The sequence represents the human lactoferrin (hLF) protein variant hLF-
CC 4N. The invention relates to novel methods of treatment using high doses
CC of lactoferrin. The methods of the invention are useful for the treatment
CC or prophylaxis of infectious diseases, inflammatory diseases and excess
CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
CC anaemia, myelopolesis, reducing reperfusion injury, cytokine release and
CC proteoglycan-mediated entry of virus into cells. The advantage of the
CC method is that the patient is substantially free of side effect responses
CC to administration of lactoferrin. Therefore large doses of lactoferrin
CC can be administered. Note: The present sequence is not shown in the
CC specification but is derived from human wild-type lactoferrin sequence
CC given in the sequence listing of the specification
XX
SQ Sequence 688 AA;
XX
Query Match 100.0%; Score 65; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AARARVWCavg 12
Db 337 AARARVWCavg 348
XX
RESULT 7
AAW71181
ID AAW71181 standard; protein; 689 AA.
XX
AC AAW71181;
XX
DT 27-OCT-1998 (first entry)
XX
DE Mutant human lactoferrin protein designated hLF-3N.
XX
KW Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
KW anti-infective; coagulant; complement activation; inhibition;
KW LPS mediated activation; myelopolesis; growth promotion;
KW intestinal epithelial cell; hydroxyl-radical formation;
KW intestinal iron uptake; excretion.
XX
OS Synthetic.

OS Homo sapiens.
XX
PN WO9833509-A2.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-IB000441.
XX
PR 03-FEB-1997; 97US-0036659P.
PR 02-FEB-1998; 98US-00017043.
XX
PA (PHAR-) PHARMING BV.
XX
PI Nuijens J, Van Berkel PHC;
XX
DR WPI: 1998-437164/37.
XX
PT Compositions containing human lactoferrin and variants - are used for
PT treating e.g. anaemia, iron-storage disease, inflammation, tumours,
PT rheumatoid arthritis, ulcerative colitis or infections.
XX
PS Claim 2; Page: 70pp; English.
XX
CC AAW7180-83 represent N-terminally truncated human lactoferrin proteins.
CC The lactoferrin variants bind heparin with lower affinity than natural
CC lactoferrin. The lactoferrin variants exhibit biological activities such
CC as anti-inflammatory, anti-viral and anti-infective activities as well as
CC a pro- and anti-coagulant effects, modulation of complement activation,
CC inhibition of LPS mediated activation of neutrophils, inhibition of
CC myelopolesis, regulation of transcription, growth promotion of intestinal
CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
CC intestinal iron uptake and excretion. note: this sequence does not appear
CC in the specification; it was created using information provided
XX
SQ Sequence 689 AA;
XX
Query Match 100.0%; Score 65; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AARARVWCavg 12
Db 338 AARARVWCavg 349
XX
RESULT 8
AAG77909
ID AAG77909 standard; protein; 689 AA.
XX
AC AAG77909;
XX
DT 22-JAN-2002 (first entry)
XX
DE Human lactoferrin variant hLF-3N.
XX
KW Human; lactoferrin; hLF; infectious disease; inflammatory disease;
KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
KW anaemia; myelopolesis; reperfusion injury; cytokine release; proteoglycan;
KW mutant; mutein; hLF-3N; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 25..28
FT /label= Cationic_domain
XX
PN WO200172322-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-NL000253.
PR 27-MAR-2000; 2000EP-00201110.


```

PR 27-MAR-2000; 2000US-0193352P.
XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX Van Bree JBM, Nuijens JH;
XX WPI; 2001-648424/74.
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
XX diseases and excess of heparin.
XX Claim 10; Page; 49pp; English.
XX The sequence represents the human lactoferrin (hLF) protein variant hLF-
XX 3N. The invention relates to novel methods of treatment using high doses
XX of lactoferrin. The methods of the invention are useful for the treatment
XX of prophyllaxis of infectious diseases, inflammatory diseases and excess
XX of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
XX anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and
XX proteoglycan-mediated entry of virus into cells. The advantage of the
XX method is that the patient is substantially free of side effect responses
XX to administration of lactoferrin. Therefore large doses of lactoferrin
XX can be administered. Note: The present sequence is not shown in the
XX specification but is derived from human wild-type lactoferrin sequence
XX given in the sequence listing of the specification
XX
SQ Sequence 689 AA;

Query Match          100.0%; Score 65; DB 4; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARARVWCAVG 12
   |||||
   |||||
   |||||
Db 338 ARARVWCAVG 349

RESULT 9
AAW71180
ID AAW71180 standard; protein; 690 AA.
XX
XX AAW71180;
AC
XX
XX 27-OCT-1998 (first entry)
DT
XX
XX Mutant human lactoferrin protein designated hLF-2N.
DE
XX
XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
XX anti-infective; coagulant; complement activation; inhibition;
XX LPS mediated activation; myelopoiesis; growth promotion;
XX intestinal epithelial cell; hydroxyl-radical formation;
XX intestinal iron uptake; excretion.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO983509-A2.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98WO-IB000441.
XX
XX 03-FEB-1997; 97US-0036859P.
XX
XX 02-FEB-1998; 98US-00017043.
XX
XX (PHAR-) PHARMING BV.
XX
XX Nuijens J, Van Berkel PHC;
XX
XX WPI; 1998-437164/37.
XX
XX Compositions containing human lactoferrin and variants - are used for
XX treating e.g. anaemia, iron-storage disease, inflammation, tumours,
XX
PT

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PT rheumatoid arthritis, ulcerative colitis or infections.
XX
XX Claim 2; Page; 70pp; English.
XX
XX AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
XX The lactoferrin variants bind heparin with lower affinity than natural
XX lactoferrin. The lactoferrin variants exhibit biological activities such
XX as anti-inflammatory, anti-viral and anti-infective activities as well as
XX a pro- and anti-coagulant effects, modulation of complement activation,
XX inhibition of LPS mediated activation of neutrophils, inhibition of
XX myelopoiesis, regulation of transcription, growth promotion of intestinal
XX epithelial cells, inhibition of hydroxyl-radical formation, and a role in
XX intestinal iron uptake and excretion. note: this sequence does not appear
XX in the specification; it was created using information provided
XX
SQ Sequence 690 AA;

Query Match          100.0%; Score 65; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARARVWCAVG 12
   |||||
   |||||
   |||||
Db 339 ARARVWCAVG 350

RESULT 10
AAG77908
ID AAG77908 standard; protein; 690 AA.
XX
XX AAG77908;
AC
XX
XX 22-JAN-2002 (first entry)
DT
XX
XX Human lactoferrin variant hLF-2N.
DE
XX
XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
XX excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
XX anaemia; myelopoiesis; reperfusion injury; cytokine release;
XX proteoglycan; hLF-2N; mutant; mutein.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Domain 26..29
XX /label= Cationic_domain

WO200172322-A2.
XX
XX 27-MAR-2001; 2001WO-NL000253.
XX
XX 27-MAR-2000; 2000EP-00201110.
XX
XX 27-MAR-2000; 2000US-0193352P.
XX
XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX
XX Van Bree JBM, Nuijens JH;
XX
XX WPI; 2001-648424/74.
XX
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
XX diseases and excess of heparin.
XX Claim 10; Page; 49pp; English.
XX
XX The sequence represents the human lactoferrin (hLF) protein variant hLF-
XX 2N. The invention relates to novel methods of treatment using high doses
XX of lactoferrin. The methods of the invention are useful for the treatment
XX or prophyllaxis of infectious diseases, inflammatory diseases and excess
XX of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
XX anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and
XX
CC

```

CC proteoglycan-mediated entry of virus into cells. The advantage of the
 CC method is that the patient is substantially free of side effect responses
 CC to administration of lactoferrin. Therefore large doses of lactoferrin
 CC can be administered. Note: The present sequence is not shown in the
 CC specification but is derived from human wild-type lactoferrin sequence
 CC given in the sequence listing of the specification

XX Sequence 690 AA;

Query Match 100.0%; Score 65; DB 4; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVVMCAVG 12
 DB 339 ARARVVMCAVG 350

RESULT 11
 ID AAG80724 standard; protein; 690 AA.

AC AAG80724;

XX 29-NOV-2002 (first entry)

XX Codon optimised lactoferrin protein.

XX Transformed plant; heterologous transcription factor; transgenic plant;
 seed protein; protein expression.

XX Homo sapiens.

PN WO200264750-A2.

PD 22-ANG-2002.

XX 14-FEB-2002; 2002WO-US004909.

PR 14-FEB-2001; 2001US-0269188P.

PR 14-FEB-2001; 2001US-0269199P.

PR 02-MAY-2001; 2001US-00847232.

XX (VENT-) VENTRIA BIOSCIENCE.

PI Huang N, Yang D;

XX WPI; 2002-657592/70.

DR N-PSDB; ABS66515.

XX Producing heterologous polypeptide in plant grain, by culturing
 PT transformed plant to form a grain-producing transforming plant; and
 PT recovering transgenic grains containing polypeptide from transformed
 PT plant.

PS Example 15; Page 117; 230pp; English.

XX The invention describes a method of producing a heterologous polypeptide
 CC (I) in a grain of a plant, comprising culturing a transformed plant (P1)
 CC comprising a first chimeric gene, and optionally, at least one
 CC heterologous transcription factor that is capable of enhancing the
 CC expression of the chimeric gene, to form a grain producing transforming
 CC plant (P2), and recovering transgenic grains containing (I) from P2. The
 CC method is useful for producing heterologous polypeptide in a grain of a
 CC plant. (I) is a non-plant storage, human or non-human animal, milk or
 CC other than a milk polypeptide, antibodies, cytokines, lymphokines,
 CC chemokines, hormones, growth factors, coagulation factors, anti-
 CC infectives, or cytotoxins, or anti-inflammatory molecule or intestinal
 CC trefoil factor (ITF) or its active fragment. Preferably, (I) is
 CC lactoferrin, lysozyme, lactoferritin, ITF, epidermal growth factor (EGF),
 CC keratinocyte growth factor (KGF), insulin-like growth factor I (IGF-I),
 CC lactonectin, kappa-casein, hapocorrin, lactoperoxidase, alpha-1-
 CC antitrypsin, immunoglobulins, alpha-lactalbumin, beta-lactoglobulin,

CC alpha-casein, beta-casein, albumin, fibrinogen or protease inhibitor.
 CC This is the amino acid sequence of a protein associated with method of
 CC producing a transgenic plant

XX Sequence 690 AA;

Query Match 100.0%; Score 65; DB 5; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVVMCAVG 12
 DB 339 ARARVVMCAVG 350

RESULT 12
 ID AAE27884 standard; protein; 690 AA.

AC AAE27884;

XX 27-DEC-2002 (first entry)

XX Human codon optimised lactoferrin.

XX Human; feed improvement; plant-derived feed; antibiotic; additive;
 XX anti-microbial; poultry; lactoferrin; flour; malt.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 319..320
 FT /note="Encoded by CTG TAC CTC"

XX WO200263975-A2.

XX 22-AUG-2002.

XX 14-FEB-2002; 2002WO-US004919.

PR 14-FEB-2001; 2001US-0269188P.

PR 02-MAY-2001; 2001US-00847232.

XX (VENT-) VENTRIA BIOSCIENCE.

PI Huang N, Rodriguez RL, Hagie FE;

XX WPI; 2002-682708/73.

DR N-PSDB; AAD45297.

XX Improved feed for production animals, comprising plant-derived feed
 PT ingredients, and seed composition containing flour, extract, or malt from
 PT mature monocot seeds and heterologous seed-produced anti-microbial
 PT proteins.

PS Example 7; Page 148-150; 175pp; English.

XX The invention relates to improved feed for production animals, comprising
 CC one or more plant-derived feed ingredients, substantially unsupplemented
 CC with small-molecule antibiotics and as an additive a seed composition
 CC containing a flour, extract or malt obtained from mature monocot seeds
 CC and one or more heterologous seed-produced anti-microbial proteins in
 CC substantially unpurified form. The invention is useful as a feed for
 CC production animals such as poultry and hoofed farm animals. The present
 CC sequence is human codon optimised lactoferrin. This sequence is used in
 CC the invention

XX Sequence 690 AA;

Query Match 100.0%; Score 65; DB 5; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARRAVVMCAVG 12
 |||||
 DB 339 ARRAVVMCAVG 350

RESULT 13
 AAY58733
 ID AAY58733 standard; protein; 692 AA.
 AC AAY58733;
 XX
 XX 25-APR-2000 (first entry)
 DT
 XX
 XX Human lactoferrin.
 DE
 XX Lactoferrin; human; transgenic plant.
 KW
 XX Homo sapiens.
 OS
 XX WO200004146-A1.
 PN
 XX 27-JAN-2000.
 PD
 XX 19-JUL-1999; 99WO-IT0000226.
 PF
 XX 17-JUL-1999; 98IT-RM000478.
 PR
 XX (PLAN-) PLANTECHNO SRL.
 PA
 XX Fogher C;
 PI
 XX WPI; 2000-161129/14.
 DR
 XX N-PSDB; AA258122.
 DX

PT Synthetic polynucleotide encoding human lactoferrin, used for production
 of functional foods, vegetal milks and human lactoferrin.
 PS Disclosure; Page 73-77; 93pp; English.

CC The present sequence is that of human lactoferrin. The invention relates
 CC to a synthetic gene (see AA258122) that encodes human lactoferrin but
 CC which has codon usage designed to maximise expression in plants.
 CC Transgenic plants that express human lactoferrin in a tissue-specific
 CC manner, especially in the seeds, can be used in processes for the
 CC production of functional vegetal milk, fruit juices, fruit and/or
 CC vegetable homogenized foods (claimed). The transgenic plants are selected
 CC from solanaceae, cereals, leguminosae, fruit bearing plants and
 CC horticultural plants, especially soybean, tobacco and rice

XX Sequence 692 AA;

Query Match 100.0%; Score 65; DB 3; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARRAVVMCAVG 12
 |||||
 DB 341 ARRAVVMCAVG 352

RESULT 14
 AAB97382
 ID AAB97382 standard; protein; 692 AA.
 AC AAB97382;
 XX
 XX 17-AUG-2001 (first entry)
 DT
 XX Human lactoferrin (hLF).
 DE
 XX Human; lactoferrin; hLF; N-terminal; antimicrobial; heparin;
 KW inflammatory response; cytokine production reduction;

KW neutrophil degranulation; myelopoiesis inhibition.
 XX Homo sapiens.
 OS
 XX

FT Key Location/Qualifiers
 FT Region 1..27
 FT /note="Fragments of the N-terminal are specifically
 FT referred to in the claims"
 FT Domain 2..5
 FT /label= Cationic_domain
 FT Domain 28..31
 FT /label= Cationic_domain

XX WO200134641-A2.
 XX 17-MAY-2001.
 XX 10-NOV-2000; 2000NO-NL000821.
 XX 11-NOV-1999; 99EP-00203775.
 XX 11-NOV-1999; 99US-0164975P.
 XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
 XX Van Berkel PHC, Nijbering PH, Nuijens JH;
 XX WPI; 2001-335909/35.
 DR
 XX

PT New polypeptides comprising the N-terminal region of human lactoferrin
 PT protein exhibit higher antimicrobial activity than the full length
 PT protein and are useful to treat bacterial infections.

XX Claim 1; Page 55-57; 59pp; English.

CC This invention relates to fragments (between 6 and 26 amino acids) of the
 CC human lactoferrin hLF protein (represented by the present sequence). N-
 CC terminal hLF peptides have antimicrobial activity. The peptides of the
 CC invention are used to treat microbial infections, especially infections
 CC by gram positive or negative bacteria, particularly listeria,
 CC Staphylococcus, Klebsiella or Escherichia species, especially L.
 CC monocytogenes, S. aureus and E. coli. Other uses include reducing
 CC inflammatory response by neutralising heparin or lipopolysaccharide or by
 CC reducing cytokine production and neutrophil degranulation, inhibiting
 CC entry of viruses such as cytomegalovirus, herpes simplex virus 1 or HIV
 CC into cells, inhibiting myelopoiesis and reducing production of GM-CSF
 CC (granulocyte/macrophage colony stimulating factor)

XX Sequence 692 AA;

Query Match 100.0%; Score 65; DB 4; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARRAVVMCAVG 12
 |||||
 DB 341 ARRAVVMCAVG 352

RESULT 15
 AAG77906
 ID AAG77906 standard; protein; 692 AA.
 AC AAG77906;
 XX
 XX 18-JAN-2002 (first entry)
 DT
 XX Human lactoferrin.
 DE
 XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
 KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
 KW anaemia; myelopoiesis; reperfusion injury; cytokine release;
 KW proteoglycan.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 2..5 /label= Cationic_domain
FT Domain 28..31 /label= Cationic_domain
FT
XX WO200172322-A2.
PN
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-NL000253.
XX
PR 27-MAR-2000; 2000EP-00201110.
PR 27-MAR-2000; 2000US-0193352P.
XX
XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX
PI Van Bree JEM, Nuijens JH;
XX
XX WPI; 2001-648424/74.
XX
XX
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
PT diseases and excess of heparin.
PT
XX
XX
PS Claim 26; Page 47-49; 49pp; English.
XX
XX
CC The sequence represents the human lactoferrin (hLF) protein. The methods
CC of the invention are useful for the treatment or prophylaxis of
CC infectious diseases, inflammatory diseases and excess of heparin e.g.
CC gastroenteritis, inflammatory bowel disease, sepsis, anaemia,
CC myeloploieses, reducing reperfusion injury, cytokine release and
CC proteoglycan-mediated entry of virus into cells. The advantage of the
CC method is that the patient is substantially free of side effect responses
CC to administration of lactoferrin. Therefore large doses of lactoferrin
CC can be administered
XX
SQ Sequence 692 AA;
Query Match 100.0%; Score 65; DB 4; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARYVMCAVG 12
|||
Db 341 ARRARYVMCAVG 352

Search completed: September 1, 2004, 00:09:43
Job time : 28.88 secs

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OW protein - protein search, using sw model

Run on: September 1, 2004, 00:04:10 ; Search time 7.76 Seconds
(without alignments)
79.834 Million cell updates/sec

Title: US-09-508-095-14

Perfect score: 65

Sequence: 1 ARRAVWCAVG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents PA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfltest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	694	3	US-08-724-586-2
2	65	100.0	694	3	US-09-421-633-2
3	65	100.0	694	4	US-09-932-190-2
4	65	100.0	705	2	US-08-655-640-2
5	65	100.0	708	2	US-08-655-640-4
6	65	100.0	709	1	US-08-154-019-2
7	65	100.0	709	1	US-08-461-333-2
8	65	100.0	709	3	US-08-464-167-2
9	65	100.0	709	3	US-09-158-313-2
10	65	100.0	709	3	US-08-476-798-2
11	65	100.0	711	1	US-08-145-681-2
12	65	100.0	711	1	US-08-250-308-2
13	65	100.0	711	1	US-08-154-019-4
14	65	100.0	711	1	US-08-461-333-4
15	65	100.0	711	1	US-08-453-703-2
16	65	100.0	711	2	US-08-456-106-2
17	65	100.0	711	3	US-08-464-167-4
18	65	100.0	711	3	US-09-158-313-4
19	65	100.0	711	3	US-08-456-108-2
20	65	100.0	711	3	US-08-476-798-4
21	65	100.0	711	3	US-09-265-577-2
22	65	100.0	711	4	US-09-633-739-2
23	65	100.0	711	5	PCT-US93-03614-2
24	58	89.2	703	1	US-08-145-681-6
25	58	89.2	703	1	US-08-453-703-6
26	58	89.2	703	2	US-08-456-106-6
27	58	89.2	703	3	US-08-456-108-6

28	58	89.2	703	3	US-09-265-577-6	Sequence 6, Appli
29	58	89.2	703	4	US-09-633-739-6	Sequence 6, Appli
30	54	83.1	708	1	US-08-145-681-4	Sequence 4, Appli
31	54	83.1	708	1	US-08-453-703-4	Sequence 4, Appli
32	54	83.1	708	2	US-08-456-106-4	Sequence 4, Appli
33	54	83.1	708	3	US-08-456-108-4	Sequence 4, Appli
34	54	83.1	708	3	US-09-265-577-4	Sequence 4, Appli
35	54	83.1	708	4	US-09-633-739-4	Sequence 4, Appli
36	42	64.6	264	4	US-09-252-991A-21445	Sequence 21445, A
37	41	63.1	884	4	US-09-252-991A-26707	Sequence 26707, A
38	39	60.0	135	4	US-09-252-991A-23456	Sequence 23456, A
39	38	58.5	25	2	US-08-464-182A-21	Sequence 21, Appli
40	38	58.5	25	2	US-08-464-182A-21	Sequence 21, Appli
41	38	58.5	30	2	US-08-464-182A-4	Sequence 4, Appli
42	38	58.5	30	2	US-08-464-182A-4	Sequence 4, Appli
43	38	58.5	47	2	US-08-464-182A-6	Sequence 6, Appli
44	38	58.5	47	2	US-08-464-182A-6	Sequence 6, Appli
45	38	58.5	50	2	US-08-693-274A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-724-586-2
Sequence 2, Application US/08724586
Patent No. 6066469
GENERAL INFORMATION:
APPLICANT: Krusel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Golinick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
TELEPHONE: (202) 638-6666
TELEFAX: (202) 638-6666
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-724-586-2
Query Match 100.0%; Score 65; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 343 ARRARVWCavg 354

RESULT 2

US-09-421-632-2
Sequence 2, Application US/09421632
Patent No. 6277817

GENERAL INFORMATION:

APPLICANT: Krutzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Golnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,586

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-421-632-2

Query Match 100.0%; Score 65; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRARVWCavg 12

Db 343 ARRARVWCavg 354

RESULT 3

US-09-932-190-2
Sequence 2, Application US/09932190
Patent No. 6455687

GENERAL INFORMATION:

APPLICANT: Krutzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Golnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.

CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/932,190
FILING DATE: 17-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-932-190-2

Query Match 100.0%; Score 65; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRARVWCavg 12

Db 343 ARRARVWCavg 354

RESULT 4

US-08-655-640-2
Sequence 2, Application US/08655640
Patent No. 5948613

GENERAL INFORMATION:

APPLICANT: Teng, Christina
APPLICANT: Panella, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992

ATTORNEY/AGENT INFORMATION:

NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581

Wed Sep 1 08:24:05 2004

us-09-508-095-14.aug31.rat

Page 3

REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-640-2

Query Match 100.0%; Score 65; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
|||||
Db 358 ARARVWCAG 369

RESULT 5
US-08-655-640-4
Sequence 4, Application US/08655640
Patent No. 5948613
GENERAL INFORMATION:
APPLICANT: Teng, Christina
APPLICANT: Panella, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, MATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-655-640-4

Query Match 100.0%; Score 65; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
|||||
Db 360 ARARVWCAG 371

RESULT 6
US-08-154-019-2
Sequence 2, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krumpfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-154-019-2

Query Match 100.0%; Score 65; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
|||||
Db 358 ARARVWCAG 369

RESULT 7
US-08-461-333-2

Sequence 2, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-333-2
Query Match 100.0%; Score 65; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 358 ARARVWCavg 369
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US-08-464-167-2
Sequence 2, Application US/08464167
Patent No. 6013857
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.

APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
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FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-167-2
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Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 358 ARARVWCavg 369
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US-09-158-313-2
Sequence 2, Application US/09158313
Patent No. 606725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/158,313
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-313-2

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Db 358 ARARVVCavg 369

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US-08-476-798-2
Sequence 2, Application US/08476798
Patent No. 6140552
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krampenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-798-2

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Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 358 ARARVVCavg 369

RESULT 11
US-08-145-681-2
Sequence 2, Application US/08145681
Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/145,681
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcgregor, Martin L.
 REGISTRATION NUMBER: 29,329
 REFERENCE/DOCKET NUMBER: 19928-0125
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713/229/1874
 TELEFAX: 713/229/1522
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 711 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: H. sapiens
 US-08-145-681-2

Query Match 100.0%; Score 65; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
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 DB 360 ARARVWCAG 371

RESULT 12
 US-08-250-308-2
 Sequence 2, Application US/08250308
 Patent No. 5571896
 Patent No. 5571896 5571896
 GENERAL INFORMATION:
 APPLICANT: Conneely, Orla M.
 APPLICANT: Heaton, Denis R.
 APPLICANT: O'Malley, Bert W.
 TITLE OF INVENTION: Production of Recombinant Human
 TITLE OF INVENTION: Lactoferrin
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski Patent Department
 STREET: 1301 McKinney St.
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77010-3095
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
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 APPLICATION NUMBER: US/08/250,308
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/873,304
 FILING DATE: 24-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler Ph.D., Benjamin A.
 REGISTRATION NUMBER: 35,423
 REFERENCE/DOCKET NUMBER: D5456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7136515246
 TELEFAX: 7136515587
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 711 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-250-308-2

Query Match 100.0%; Score 65; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
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 DB 360 ARARVWCAG 371

RESULT 13
 US-08-154-019-4
 Sequence 4, Application US/08154019
 Patent No. 5633076
 GENERAL INFORMATION:
 APPLICANT: Deboer, Herman A.
 APPLICANT: Strijker, Rein
 APPLICANT: Heyneker, Herbert L.
 APPLICANT: Platenburg, Gerald
 APPLICANT: Lee, Sang He
 APPLICANT: Pieper, Frank
 APPLICANT: Krimpenfort, Paul J.A.
 TITLE OF INVENTION: Production of Recombinant Polypeptides
 TITLE OF INVENTION: by Bovine Species and Transgenic Methods
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/154,019
 FILING DATE: 16-NOV-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/461,333
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/077,788
 FILING DATE: 15-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/895,956
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/619,131
 FILING DATE: 27-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/444,745
 FILING DATE: 01-DEC-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebescheutz, Joe O.
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 16994-003123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 711 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-154-019-4

Query Match 100.0%; Score 65; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 12
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DB 360 ARRAVWCAVG 371

RESULT 14
US-08-461-333-4
Sequence 4, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-333-4

Query Match 100.0%; Score 65; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 360 ARRAVWCAVG 371

RESULT 15
US-08-453-703-2
Sequence 2, Application US/08453703
Patent No. 5766939
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: H. sapiens
US-08-453-703-2

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Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 360 ARRAVWCAVG 371

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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3	65	100.0	630	14	US-10-077-331-4	Sequence 4, Appl1
4	65	100.0	650	16	US-10-633-835-4	Sequence 4, Appl1
5	65	100.0	694	13	US-10-023-036-2	Sequence 2, Appl1
6	65	100.0	709	14	US-10-170-221-2	Sequence 2, Appl1
7	65	100.0	711	14	US-10-169-297-9	Sequence 9, Appl1
8	65	100.0	711	14	US-10-170-221-4	Sequence 4, Appl1
9	65	100.0	711	15	US-10-341-434-202	Sequence 202, Appl1
10	65	100.0	711	15	US-10-341-434-218	Sequence 218, Appl1
11	65	100.0	711	15	US-10-408-763A-68	Sequence 69, Appl1
12	65	100.0	711	16	US-10-408-763A-2000	Sequence 2000, Appl1
13	64	83.1	234	14	US-10-169-297-35	Sequence 35, Appl1
14	54	83.1	708	14	US-10-169-297-8	Sequence 8, Appl1
15	46	70.8	77	9	US-09-738-626-3901	Sequence 3901, Appl1

16	44	60	16	US-10-437-963-147215	Sequence 147215, App
17	43	705	16	US-09-847-208-103	Sequence 103, App
18	66.2	77	16	US-10-437-963-105618	Sequence 105618, App
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45	37	56.9	16	US-10-437-963-105618	Sequence 105618, App

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RESULT 1
US-10-169-297-49
; Sequence 49, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
; APPLICANT: TORDIN, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; TITLE OF INVENTION: Hepatitis
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/JP00/09393
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 11/374087
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-169-297-49

Query Match      100.0%; Score 65; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

CY      1  ARRAAYVVCAGV 12
      |||||
Db      114  ARRAAYVVCAGV 125

```

GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Feed Additive Compositions and Methods
FILE REFERENCE: 50665-8021.US00
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-816-4

Query Match 100.0%; Score 65; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGV 12
Db 339 ARARVWCAGV 350

RESULT 3
US-10-077-381-4
Sequence 4, Application US/10077381
Publication No. US20030074700A1
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Expression of Human Milk Proteins in
FILE REFERENCE: 50665-8022.US00
CURRENT APPLICATION NUMBER: US/10/077,381
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,199
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-10-077-381-4

Query Match 100.0%; Score 65; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGV 12
Db 339 ARARVWCAGV 350

RESULT 4
US-10-639-835-4

Sequence 4, Application US/10639835
Publication No. US20040111766A1
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Expression of Human Milk Proteins in
FILE REFERENCE: 50665-8022.US01
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: US 10/077,381
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,199
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-10-639-835-4

Query Match 100.0%; Score 65; DB 16; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGV 12
Db 339 ARARVWCAGV 350

RESULT 5
US-10-023-096-2
Sequence 2, Application US/10023096
Publication No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Krutzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409

Wed Sep 1 08:24:05 2004

us-09-508-095-14.aug31.rapb

Page 3

REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 100.0%; Score 65; DB 13; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.008; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 ARARVWCavg 12
DB 343 ARARVWCavg 354

RESULT 6
US-10-170-221-2
Sequence 2, Application US/10170221
Publication No. US20030192068A1
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170.221
FILING DATE: 11-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-221-2

Query Match 100.0%; Score 65; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCavg 12
DB 358 ARARVWCavg 369

RESULT 7
US-10-169-297-9
Sequence 9, Application US/10169297
Publication No. US20030171276A1
GENERAL INFORMATION:
APPLICANT: Murata, Masashi
Enjoji, Takashi
APPLICANT: Tohdoh, Naoki
TITLE OF INVENTION: Preventives and Remedies for Chronic
Hepatitis
FILE REFERENCE: 3435.1000-000
CURRENT FILING DATE: 2002-10-31
CURRENT APPLICATION NUMBER: US/10/169,297
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: PCT/JP00/09393
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 711
TYPE: prf
ORGANISM: Homo sapiens
US-10-169-297-9
Query Match 100.0%; Score 65; DB 14; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARARVWCavg 12
DB 360 ARARVWCavg 371
RESULT 8
US-10-170-221-4
Sequence 4, Application US/10170221
Publication No. US20030192068A1
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170,221
FILING DATE: 11-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/077,788
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US/07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US/07/619,131
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: US/07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-170-221-4

Query Match 100.0%; Score 65; DB 14; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
DB 360 ARARVWCAG 371

RESULT 9
US-10-341-434-202
Sequence 202, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 202
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-202

Query Match 100.0%; Score 65; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
DB 360 ARARVWCAG 371

RESULT 10
US-10-341-434-218
Sequence 218, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 218
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-218

Query Match 100.0%; Score 65; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
DB 360 ARARVWCAG 371

RESULT 11
US-10-440-464-69
Sequence 69, Application US/10440464
Publication No. US20040018528A1
GENERAL INFORMATION:
APPLICANT: DEPRIMO, SAMUEL
APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: MORIMOTO, AYESA
APPLICANT: SMOLICH, BEVERLY
APPLICANT: MANNING, WILLIAM
APPLICANT: WALTER, SARAH
APPLICANT: CHERRINGTON, JULIE
APPLICANT: SCHILLING, JIM
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
FILE REFERENCE: 038602/1592
CURRENT APPLICATION NUMBER: US/10/440,464
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: 60/448,874
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-440-464-69

Query Match 100.0%; Score 65; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12
DB 360 ARARVWCAG 371


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RESULT 12
US-10-408-765A-2000
; Sequence 2000, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Goshu, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale F.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2000
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2000

Query Match      100.0%; Score 65; DB 16; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ARARVWCavg 12
Db      360 ARARVWCavg 371

RESULT 13
US-10-169-297-35
; Sequence 35, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
; APPLICANT: Tomoda, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; TITLE OF INVENTION: Hepatitis
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/JP00/09393
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 11/374087
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-169-297-35

Query Match      83.1%; Score 54; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ARARVWCavg 12
Db      71  ARYRVWCavg 82

RESULT 14
US-10-169-297-8
; Sequence 8, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Tomoda, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; TITLE OF INVENTION: Hepatitis
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/JP00/09393
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 11/374087
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-169-297-8

Query Match      83.1%; Score 54; DB 14; Length 708;
Best Local Similarity 83.3%; Pred. No. 0.64;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ARARVWCavg 12
Db      359 ARYRVWCavg 370

RESULT 15
US-09-738-626-3901
; Sequence 3901, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3901
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3901

Query Match      70.8%; Score 46; DB 9; Length 77;
Best Local Similarity 72.7%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  RRARVWCavg 12
Db      29 RRLRTWCavg 39

Search completed: September 1, 2004, 00:49:18
Job time : 29.36 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:03:45; Search time 6.96 Seconds
(without alignments)

165,847 Million cell updates/sec

Title: US-09-508-095-14

Perfect score: 65

Sequence: 1 ARARVWCAVG 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues.

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	711	1	TFHUL
2	58	89.2	703	2	A45543
3	54	83.1	708	1	TFBOL
4	53	81.5	708	2	JC2323
5	52	80.0	707	1	A28438
6	44	67.7	704	2	I47228
7	43	66.2	705	1	TFCHB
8	40	61.5	260	2	E81185
9	40	61.5	436	2	T36706
10	39.5	60.8	129	2	C87219
11	39	60.0	285	1	IDECRP
12	39	60.0	285	2	I64780
13	39	60.0	350	2	E87327
14	39	60.0	350	2	E87327
15	39	60.0	350	2	E87327
16	39	60.0	350	2	E87327
17	38	58.5	126	2	D71330
18	38	58.5	150	2	T08220
19	38	58.5	330	2	AG3650
20	38	58.5	337	2	B71340
21	38	58.5	383	2	G83500
22	38	58.5	386	2	G97316
23	38	58.5	437	2	B82778
24	38	58.5	483	2	H87492
25	38	58.5	505	2	B81021
26	38	58.5	505	2	C81965
27	38	58.5	699	2	AB3031
28	38	58.5	765	2	B88254
29	37	56.9	176	2	F72563

30	37	56.9	203	2	JC7521	ribosomal protein
31	37	56.9	307	2	AE3466	maltose transport
32	37	56.9	326	2	A85435	hypothetical prote
33	37	56.9	706	2	S33761	transferrin precu
34	37	56.9	1099	2	A59321	myosin VIII ZMW3
35	36	55.4	108	2	F72507	hypothetical prote
36	36	55.4	134	2	T45188	hypothetical prote
37	36	55.4	221	2	C34768	ORF2 protein - Ort
38	36	55.4	328	2	JE0375	carbonic anhydrase
39	36	55.4	449	2	H70526	probable cytochrom
40	36	55.4	477	2	D83617	probable amino aci
41	36	55.4	497	2	T48676	proline uptake pro
42	36	55.4	512	2	E89978	high affinity prol
43	36	55.4	696	1	S01384	transferrin - pig
44	36	55.4	827	2	H83217	probable transcrip
45	36	55.4	987	2	AF2296	hypothetical prote

ALIGNMENTS

RESULT 1
lactotransferrin precursor (validated) - human
N/Alternate names: lactoferrin
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
R/Cho: Y.
submitted to the EMBL Data Library, March 1994
A/Reference number: G06820
A/Accession: G01394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-711 <CHO>
A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237
N/Ref: M.W. Moloshuk, S.L. deBoer, H.A. Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A/Reference number: S11228; MUID:90384839; PMID:2402455
A/Accession: S11228
A/Molecule type: mRNA
A/Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>
A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CA37914.1; PID:G34416
R/Feng, C.T., Liu, Y., Yang, N., Walmer, D., Pannell, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A/Title: Differential molecular mechanism of the estrogen action that regulates lactofe
A/Reference number: A45401; MUID:93125571; PMID:1480183
A/Accession: A45401
A/Molecule type: DNA
A/Residues: 1-15 <TEN>
A/Cross-references: GB:S52653; NID:G263311; PIDN:AA824877.1; PID:G263312
A/Experimental source: placenta (NCBIP:122202)
R/Powell, M.J., Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A/Title: Nucleotide sequence of human lactoferrin cDNA.
A/Reference number: S10324; MUID:90326549; PMID:2374734
A/Accession: S10324
A/Molecule type: mRNA
A/Residues: 3-711 <POW>
A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CA37116.1; PID:G34412
R/Stowell, J., K.M., Rado, T.A., Funk, W.D., Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A/Reference number: S15853; MUID:91264786; PMID:2043066
A/Accession: S15853
A/Molecule type: mRNA
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Residues: 20-31 <ST1>
A/Accession: S20841
A/Molecule type: protein
A/Residues: 20-28, 'X', 30-31 <ST2>

R:Rado, T.A.; Mel, X.; Benz Jr., E.J.
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A:Reference number: 507160; PMID:8801031; PMID:3477390
 A:Accession: 507160
 A:Molecule type: mRNA
 A:Residues: 436-487, 'A', 489-711 <RAD>
 A:Cross-references: EMBL:M8642; NID:g186815; PIDD:AAA8665.1; PID:g386855
 R:Benella, T.O.; Liu, Y.; Huang, A.T.; Teng, C.T.
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; PMID:91235214; PMID:1674448
 A:Accession: A61169
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 3-701, 'SWKPVN' <PAN>
 A:Experimental source: normal breast tissue
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoengen, F.; Legendre, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1994
 A:Title: Human lactoferrin: amino acid sequence and structural comparisons with other
 A:Reference number: A31000; PMID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140, '142-169, 171-203, 'V', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A:Note: this is the final paper in a series
 R:Houen, G.; Hoegdall, B.V.; Barkholt, V.; Norrskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A:Reference number: S74119; PMID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:LTF
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/DNA: signal sequence #status predicted <SIG>
 F:20-711/Product: lactoferrin #status experimental <MNT>
 F:21-356/DNA: transferrin repeat homology <TRH1>
 F:356-699/DNA: transferrin repeat homology <TRH2>
 F:39-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat
 Query Match 100.0%; Score 65; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 DB 360 ARARVWCAVG 371

RESULT 2

A:Accession: A45543
 A:Title: Lactoferrin precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 17-Feb-1994 #sequence _revision 17-Feb-1994 #text _change 04-Mar-2000
 C:Accession: A45543; S24173
 R:Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A:Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A:Reference number: A45543; PMID:92367939; PMID:1503259
 A:Accession: A45543
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-703 <ALB>
 A:Experimental source: mammary gland
 A:Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:111153)
 R:Lydon, C.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Conneely, O.M.

Biochim. Biophys. Acta 1132, 97-99, 1992
 A:Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A:Reference number: S24173; PMID:92379101; PMID:1511016
 A:Accession: S24173
 A:Molecule type: mRNA
 A:Residues: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
 A:Cross-references: EMBL:M92089; NID:g164613; PIDD:AAA31102.1; PID:g164614
 A:Experimental source: mammary gland
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/DNA: signal sequence #status predicted <SIG>
 F:20-703/Product: lactoferrin #status predicted <MNT>
 F:20-350/DNA: transferrin repeat homology <TRH1>
 F:356-48/Region: antimicrobial
 F:354-691/DNA: transferrin repeat homology <TRH2>
 F:28-62, 38-53, 129-212, 171-187, 184-195, 245-259, 362-394, 372-385, 419-698, 439-661, 471-546, 49
 F:77, 107, 206, 267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:135/Binding site: carbonate (Arg) #status predicted
 F:409, 447, 540, 609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Asn) (covalent) #status predicted
 F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.2%; Score 58; DB 2; Length 703;
 Best Local Similarity 83.3%; Pred. No. 0.018;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 DB 354 ARARVWCAVG 365

RESULT 3

TFBOI

A:Title: Lactoferrin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Mar-1992 #sequence _revision 21-Nov-1997 #text _change 11-May-2000
 C:Accession: A45919; S14674; S14110; S18517; J70595; S13097; S18518; S13881; P10148; S21
 F:Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 PNAS 91, 6233, 1994
 A:Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein from
 A:Reference number: A45919
 A:Accession: A45919
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-708 <TSA>
 A:Cross-references: GB:U08604; NID:g163269; PIDD:AAA0609.1; PID:g163270
 R:Pierce, A.
 Submitted to the EMBL Data Library, November 1990
 A:Reference number: S14674
 A:Accession: S14674
 A:Molecule type: mRNA
 A:Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PII>
 A:Cross-references: EMBL:X57084; NID:g505; PIDD:CAA40366.1; PID:g506
 R:Pierce, A.; Colavizza, D.; Benaisse, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A:Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A:Reference number: S14110; PMID:9160550; PMID:2001696
 A:Accession: S14110
 A:Molecule type: mRNA
 A:Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PII>
 A:Cross-references: EMBL:X57084
 A:Accession: S18517
 A:Molecule type: protein
 A:Residues: 20-35, 182-114, 148-163, 'P', 166-178, 'V', 'P', 183-190, 205-212, 230-239, 304-339, 59
 R:Goodman, R.E.; Schandacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A:Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
 A:Reference number: J70595; PMID:9202896; PMID:1718261
 A:Accession: J70595
 A:Molecule type: mRNA
 A:Residues: 1-65, 'PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A:Cross-references: GB:M63502

A>Note: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 R.Mead, P.E.; Tweedie, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A>Title: cDNA and protein sequence of bovine lactoferrin.
 A:Reference number: S13097; MUID:91088328; PMID:2263492
 A:Accession: S13097
 A:Molecule type: mRNA
 A:Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A:Accession: S18518
 A:Molecule type: protein
 A:Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586;587-589;598-619
 R.Mead, P.E.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S13881
 A:Accession: S13881
 A:Molecule type: mRNA
 A:Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
 A:Cross-references: EMBL:X54801
 R.Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A>Title: Purification and characterization of bovine lactoferrin from secretions of the
 A:Reference number: P10148; MUID:90031466; PMID:2805645
 A:Accession: P10148
 A:Molecule type: protein
 A:Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R.Bellamy, W.; Takase, M.; Yanaguchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A>Title: Identification of the bactericidal domain of lactoferrin.
 A:Reference number: S21756; MUID:92287941; PMID:1599334
 A:Accession: S21756
 A:Molecule type: protein
 A:Residues: 36-60 <BEL>
 R.Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A>Title: Separation and characterization of the C-terminal half molecule of bovine lacto
 A:Reference number: A56659; MUID:93253156; PMID:8486645
 A:Accession: A56659
 A:Molecule type: protein
 A:Residues: 20-25;302-308;359-366, 'X', 368-376, 'X', 378 <SHI>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-708/Product: lactotransferrin #status experimental <MAT>
 F:20-355/Domain: transferrin repeat homology <TRH>
 F:36-60/Region: antimicrobial
 F:359-596/Domain: transferrin repeat homology <TRH2>
 F:28-64;134-217;176-192;179-200;189-202;250-264;367-399;377-390;424-703;444-666;476-551,
 F:38-55/Dsulfide bonds: #status predicted
 F:79,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:140/Binding site: carbonate (Arg) #status experimental
 F:252;300;387;495;564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:414;452;545;614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:482/Binding site: carbonate (Arg) #status experimental

Query Match 83.1%; Score 54; DB 1; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.091;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 |||||
 DB 359 ARYTRVWCAVG 370

RESULT 4
 JC2323
 lactoferrin - goat
 C/Species: Capra aegagrus hircus (domestic goat)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C/Accession: JC2323
 R:De Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus

A:Reference number: JC2323; MUID:94380047; PMID:8093048
 A:Accession: JC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252;300;387;495;564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.5%; Score 53; DB 2; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 |||||
 DB 359 ARCTRVWCAVG 370

RESULT 5
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: A28438; A41205
 R:Penhagost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R.Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <Liu>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.0%; Score 52; DB 1; Length 707;
 Best Local Similarity 75.0%; Pred. No. 0.21;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 |||||
 DB 358 ASKARVWCAVG 369

RESULT 6
 I47228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
 C/Accession: I47228
 R:Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from poi
 A:Reference number: I47228; MUID:93099129; PMID:1463741
 A:Accession: I47228
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-704 <ROU>
 A:Cross-references: EMBL:U36916; NID:g1016329; PIDN:AAB58956.1; FID:g1016330
 C/Genetics:

A:Gene: PLCA
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication
 F:/20-350/Domain: transferrin repeat homology <TRH>

Query Match 67.7%; Score 44; DB 2; Length 704;
 Best Local Similarity 87.5%; Pred. No. 5.3;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RYRWCAVG 12
 Db 356 RYRWCAVG 363

RESULT 7

TFCH

Overtransferrin precursor - chicken
 N:Alternate names: conalbumin; transferrin
 C:Species: Gallus gallus (chicken)

C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: A26845; A91115; A92229; A91116; A40674; B61573; A90282; S02476; A03262
 R:Uetlich, J.M.; Hen, R.; Marteaux, L.; Garner, J.M.; Chambon, P.
 Nucleic Acids Res. 15, 7643-7645, 1987

A:Title: Sequence of the chicken ovotransferrin gene.
 A:Reference number: A26845; MUID:88015626; PMID:3658709

A:Accession: A26845
 A:Molecule type: DNA

A:Residues: 1-705 <DB1>
 A:Cross-references: GB:Y00407; NID:963111; PIDN:CA66468.1; PID:G295721
 R:Uetlich, J.M.; Chambon, P.

Eur. J. Biochem. 122, 291-295, 1982
 A:Title: The complete nucleotide sequence of the chicken ovotransferrin mRNA.
 A:Reference number: A91115; MUID:82138851; PMID:7060577

A:Accession: A91115
 A:Molecule type: mRNA

A:Residues: 1-82; 'V', 84-99; 'T', 101-153; 'W', 155-238; 'LN', 241-685; 'N', 687-705 <DB2>
 A:Cross-references: EMBL:X02009

A:Note: The codons given for residues 132 (AAC) and 317 (UUC) are inconsistent with the
 R:Uetlich, J.M.; Lee, D.C.; Palmiter, R.D.

J. Biol. Chem. 253, 3771-3774, 1978
 A:Title: Identical precursors for serum transferrin and egg white conalbumin.
 A:Reference number: A92229; MUID:78171533; PMID:649604

A:Accession: A92229
 A:Molecule type: protein

A:Residues: 1-23 <TRH>
 R:Williams, J.; Ellemann, T.C.; Kingston, I.B.; Wilkins, A.G.; Kuhn, K.A.

Eur. J. Biochem. 122, 297-303, 1982
 A:Title: The primary structure of hen ovotransferrin
 A:Reference number: A91116; MUID:82138852; PMID:695872

A:Accession: A91116
 A:Molecule type: protein

A:Residues: 1-50; 154-82; 'V', 84-92; 102-146; 162-168; 170-228; 241-283; 289-333; 338-344; 350-351
 R:Gentili, C.; Bianco, P.; Neri, M.; Malpelli, M.; Campanile, G.; Castagnola, P.; Cancedo

J. Cell Biol. 122, 703-712, 1993
 A:Title: Cell proliferation, extracellular matrix mineralization, and ovotransferrin tra

A:Reference number: A40674; MUID:93328771; PMID:8393014
 A:Accession: A40674

A:Molecule type: protein
 A:Residues: 20-28; 'X', 30-38; 'X', 40-44 <GEN>

R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991

A:Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
 A:Reference number: A61573; MUID:91293379; PMID:2065820

A:Accession: B61573
 A:Molecule type: protein

A:Residues: 20-28; 'X', 30-38; 'X', 40-43; 'S' <CHD>
 R:Kingston, I.B.; Williams, J.

Biochem. J. 147, 463-472, 1975
 A:Title: The amino acid sequence of a carbohydrate-containing fragment of hen ovotransferrin

A:Reference number: A90282; MUID:76039467; PMID:1172663
 A:Accession: A90282

A:Molecule type: protein

A:Residues: 480-582 <KIN>
 R:Ellemann, T.C.; Williams, J.

Biochem. J. 116, 515-532, 1970
 A:Title: The amino acid sequences of cysteine acid-containing peptides from performic acid

A:Reference number: A90246; MUID:70141846; PMID:4907959
 A:Contents: annotation; disulfide bonds

R:Williams, J.; Moreton, K.
 Biochem. J. 251, 849-855, 1988

A:Title: The dimerization of half-molecule fragments of transferrin.
 A:Reference number: S02476; MUID:88326225; PMID:3415649

A:Accession: S02476
 A:Molecule type: protein

A:Residues: 20-23; 295-302; 336-366; 674-679; 'T', 681; 'F', 683-685; 'N', 687-705 <WT2>
 C:Comment: Ovotransferrin (conalbumin) and transferrin have identical protein components

rin is synthesized in the liver.
 C:Comment: Ovotransferrin has a bacteriostatic function. Its concentration in avian egg

C:Comment: Plasma apotransferrin promotes the oxidation of ferrous ions, which would oth

C:Comment: In electrophoretic and genetic studies, transferrin shows strong polymorphism

C:Genetics: Amino acids: 15/1; 69/3; 106/1; 170/1; 215/2; 234/1; 290/3; 353/1; 404/3; 436/1; 448/1; 50

C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; egg white; glycoprotein; iron binding; plasma

F:/20-705/Product: transferrin #status experimental <SIG>
 F:/21-355/Domain: transferrin repeat homology <TRH>

F:/23-64, 134-216, 178-193, 190-201, 247-261, 367-399, 424-659, 440-662, 473-549, 497-690/Disulfid

F:/39-55, 377-390, 589-603/Disulfide bonds: #status predicted
 F:/499/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F:/507-521, 518-532/Disulfide bonds: (or 507-518, 521-532) #status predicted

Query Match 66.2%; Score 43; DB 1; Length 705;
 Best Local Similarity 63.6%; Pred. No. 8;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RYRWCAVG 12
 Db 360 RYRWCAVG 370

RESULT 8

Chol-disulfide interchange protein dbc homolog NMB0550 [imported] - Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
 C:Accession: E81185; D81916

R:Terrellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Hatt, D.R.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
 Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ven
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: E81185

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-260 <DET>
 A:Cross-references: GB:AE002411; GB:AE002098; NID:G7225776; PIDN:AA40979.1; PID:G722577

A:Experimental source: serogroup B, strain MC58
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raftery, R.;
 Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: D81916
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-260 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; NID:G7379424; PIDN:CA84014.1; PID:G737945
 A:Experimental source: serogroup A, strain Z2491

C:Genetics:
 A:Gene: NMB0550; NMA0730

Query Match 61.5%; Score 40; DB 2; Length 260;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARVWC 9
DB 181 ARKAQILWC 189

RESULT 9
T36706
hypothetical protein SCH69.07c - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T36706
R/Murphy, L.; Harrie, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A/Reference number: Z21612
A/Accession: T36706
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-436 <MUR>
A/Cross-references: EMBL:AL079308; PIDN:CAB45204.1; GSPDB:GN00070; SCOEDB:SCHE9.07C
C/Genetics: A/Experimental source: strain A3(2)
A/Genes: SCOEDB:SCHE9.07c

Query Match 61.5%; Score 40; DB 2; Length 436;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 0; Indels 18; Gaps 1;

QY 1 ARRAR-----VWCVAG 12
DB 153 ARRARAAARAGGERVEDRVGPMVLCALG 182

RESULT 10
C87219
hypothetical protein [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: C87219
R/Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Dutroy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sg
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:2118732; PMID:11234002
A/Accession: C87219
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-129 <STO>
A/Cross-references: GB:AL450380; NID:G13094034; PIDN:CAC31995.1; GSPDB:GN00147
C/Genetics: A/Genes: ML2478

Query Match 60.8%; Score 39.5; DB 2; Length 129;
Best Local Similarity 60.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 ARR---ARVWCVAG 12
DB 51 ARRVDFARAGMCTVVG 65

RESULT 11
IDECRP
replication initiation protein - Escherichia coli plasmids
C/Species: Escherichia coli
C/Date: 18-Dec-1991 #sequence_revision 17-Dec-1992 #text_change 16-Jul-1999
C/Accession: A03602; B03602; S01773; S05591; A48662; C28378; I41109
R/Rosen, J.; Ryder, T.; Inokuchi, H.; Ohtsubo, H.; Ohtsubo, E.

Mol. Gen. Genet. 179, 527-537, 1980
A/Title: Genes and sites involved in replication and incompatibility of an R100 plasmid
A/Reference number: A93119; MUID:81074309; PMID:7003300
A/Accession: A03602
A/Molecule type: DNA
A/Residues: 1-285 <ROI>
A/Cross-references: GB:J01762; GB:J01761; GB:J01767; GB:J01768; NID:G151740; PIDN:AAA922
A/Experimental source: plasmid R100
R/Rosen, J.; Ryder, T.; Ohtsubo, H.; Ohtsubo, E.
Nature 290, 794-797, 1981
A/Title: Role of RNA transcripts in replication incompatibility and copy number control
A/Reference number: A93253; MUID:81173118; PMID:6163994
A/Accession: B03602
A/Molecule type: DNA
A/Residues: 1-77 <ROS>
A/Experimental source: plasmid R1
R/Dong, X.; Womble, D.D.; Rownd, R.H.
J. Mol. Biol. 202, 495-509, 1988
A/Title: In-vivo studies on the cis-acting replication initiator protein of IncFII plasm
A/Reference number: S01773; MUID:85011975; PMID:3050127
A/Accession: S01773
A/Molecule type: DNA
A/Residues: 1-285 <DON>
A/Cross-references: EMBL:X12776; NID:G42707; PIDN:CAA31263.1; PID:G581213
A/Experimental source: plasmid NR1
R/Maesi, H.; Arai, K.I.
Nucleic Acids Res. 16, 6493-6514, 1988
A/Title: RepA protein- and oriR-dependent initiation of R1 plasmid replication: identifi
A/Reference number: S05591; MUID:88289416; PMID:3041379
A/Accession: S05591
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 270-285 <MAS>
A/Cross-references: EMBL:X12587; NID:G41107; PIDN:CAA31100.1; PID:G41108
A/Experimental source: plasmid R1
R/Jiang, T.; Min, Y.N.; Liu, W.; Womble, D.D.; Rownd, R.H.
J. Bacteriol. 175, 5350-5358, 1993
A/Title: Insertion and deletion mutations in the repA4 region of the IncFII plasmid NR1
A/Reference number: A48662; MUID:93374826; PMID:8396115
A/Accession: A48662
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 252-285 <JIA>
A/Experimental source: plasmid NR1
R/Dong, X.; Womble, D.D.; Rownd, R.H.
J. Bacteriol. 169, 5353-5363, 1987
A/Title: Transcriptional pausing in a region important for plasmid NR1 replication conti
A/Reference number: A28378; MUID:88058738; PMID:2445727
A/Accession: C28378
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-50 <DO2>
R/Womble, D.D.; Sampathkumar, P.; Easton, A.M.; Luckow, V.A.; Rownd, R.H.
J. Mol. Biol. 181, 395-410, 1985
A/Title: Transcription of the replication control region of the IncFII R-plasmid NR1 in
A/Accession: I41109
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-285 <RES>
A/Cross-references: EMBL:X02302; NID:G42132; PIDN:CAA26168.1; PID:G581144
C/Genetics: A/Genes: repA
A/Genome: plasmid
A/Start codon: GTG
C/Suprafamily: repl protein
C/Keywords: plasmid copy control

Query Match 60.0%; Score 39; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARVWC 9

Db 168 ARRSRYVM 175

RESULT 12

164780
 replication-associated protein A1 - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 26-Aug-1999
 C:Accession: 164780; 14110
 R:Ohtsubo, H.; Ryder, T.B.; Maeda, Y.; Armstrong, K.A.; Ohtsubo, E.
 Adv. Biophys. 21, 115-133, 1986
 A>Title: DNA replication of the resistance plasmid R100 and its control.
 A:Reference number: 151821; PMID:86319522; PMID:3019092
 A:Accession: 164780
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-285 <RES>
 A:Cross-references: GB:M26840; NID:g151770; PIDN:AAA6067.1; PID:g151773
 R:Nomb, D.D.; Sampathkumar, P.; Easton, A.M.; Luckow, V.A.; Rownd, R.H.
 U. Mol. Biol. 181, 395-410, 1985
 A>Title: Transcription of the replication control region of the IncF1 R-plasmid NR1 in
 A:Reference number: 141106; PMID:85160860; PMID:2580099
 A:Accession: 141110
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: M', 166-285 <RES>
 A:Cross-references: EMBL:X02302; NID:g42132; PIDN:CAA26169.1; PID:g581145
 C:Superfamily: repl protein

Query Match

Best Local Similarity 60.0%; Score 39; DB 2; Length 285;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVVM 8
 Db 168 ARRSRYVM 175

RESULT 13

E87327
 hypothetical protein CC0632 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: E87327
 R:Nierman, W.C.; Fejdyjym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, U.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; PMID:21173698; PMID:11259647
 A:Accession: E87327
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <STO>
 A:Cross-references: GB:AE005673; NID:g13421843; PIDN:AAK2617.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0632

Query Match

Best Local Similarity 60.0%; Score 39; DB 2; Length 350;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ARVVMCAVG 12
 Db 45 ARVVMCAVG 53

RESULT 14

T46684
 p-hydroxybenzaldehyde dehydrogenase [imported] - Pseudomonas putida plasmid pRA4000
 C:Species: Pseudomonas putida
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000

C:Accession: T46684
 R:Cronin, C.N.; Kim, J.H.; Fuller, J.; Zhang, X.P.; McIntire, W.S.
 DNA Seq. 10, 7-17, 1999
 A>Title: Organization and sequences of p-hydroxybenzaldehyde dehydrogenase and other pla

659.
 A:Reference number: Z23132; PMID:20029269; PMID:10565539

A:Accession: T46684
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-491 <CRO>
 A:Cross-references: EMBL:U96338; NID:g4808503; PIDN:AAA75634.2; PID:g4808506

A:Experimental source: NCIMB 9866

C:Genetics:
 A:Gene: pchA

A:Genome: plasmid pRA4000
 A:Function:
 A:Description: catalyzes oxidation of p-hydroxybenzaldehyde to p-hydroxybenzoic acid

A>Note: cofactor NADP+

C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 60.0%; Score 39; DB 2; Length 491;
 Best Local Similarity 58.3%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARRAVVMCAVG 12
 Db 58 ARRAVVMCAVG 69

RESULT 15

T23526
 hypothetical protein K09A11.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T23526
 R:Coles, L.

submitted to the EMBL Data Library, August 1995
 A:Reference number: Z19752

A:Accession: T23526
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-549 <WIL>
 A:Cross-references: EMBL:Z50742; PIDN:CAA90618.1; GSPDB:GN00028; CESP:K09A11.5

A:Experimental source: clone K09A11

C:Genetics:
 A:Gene: CESP:K09A11.5

A:Map position: X
 A:Introns: 20/3; 57/3; 165/3; 199/1; 242/1; 274/1; 310/1; 423/1; 460/3; 494/2; 516/2

Query Match 60.0%; Score 39; DB 2; Length 549;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRAVVMCAVG 9
 Db 57 ARRAVVMCAVG 65

Search completed: September 1, 2004, 00:17:00
 Job time : 9.36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:44 ; Search time 4.08 Seconds
(without alignments)
153.148 Million cell updates/sec

Title: US-09-508-095-14

Perfect score: 65
Sequence: 1 AARRAVWCavg 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	708	1 TRFL_BUBBU	O77698 bubalus bub
2	65	100.0	711	1 TRFL_HUMAN	P02788 homo sapien
3	60	92.3	695	1 TRFL_HORSE	O77811 equus caball
4	58	89.2	704	1 TRFL_PIG	P14632 sus scrofa
5	57	87.7	708	1 TRFL_CAMDR	Q14632 camelus dro
6	54	83.1	708	1 TRFL_BOVIN	P24627 bos taurus
7	53	81.5	708	1 TRFL_CAPI	O29477 capra hircu
8	52	80.0	707	1 TRFL_MOUSE	P08071 mus musculu
9	44	67.7	704	1 ICA_PIG	Q93545 sus scrofa
10	43	66.2	705	1 TRFE_CHICK	P02789 gallus gall
11	40	61.5	686	1 TRFE_ANAPL	P66410 anas platyr
12	39	60.0	285	1 REP2_ECOLI	P03066 escherichia
13	38	58.5	870	1 CSX2_SCHRO	O95b03 aeropyrum p
14	37	56.9	176	1 YH92_ABRSE	P27428 equus caball
15	37	56.9	706	1 TRFE_HORSE	O75439 homo sapien
16	36	55.4	328	1 CAHB_HUMAN	O08447 mus scrofa
17	36	55.4	449	1 C13A_MYCTU	P09571 sus scrofa
18	36	55.4	666	1 TRFE_PIG	P17901 mycobacteri
19	35	53.8	174	1 YN11_MYCTU	O94943 rickettsia
20	35	53.8	220	1 Y231_RICPR	P70795 agrobacteri
21	35	53.8	502	1 Y22R_AGRVI	O92079 gadus morhu
22	35	53.8	642	1 TRFE_GADVI	P79819 oncorhynch
23	35	53.8	687	1 TRFE_ONCKI	P80426 salmo salar
24	35	53.8	690	1 TRFE_SALSA	P79819 oncorhynch
25	35	53.8	690	1 TRFE_ORYLA	P79819 oncorhynch
26	35	53.8	691	1 TRFE_SALSA	P79819 oncorhynch
27	35	53.8	704	1 TRFE_BOVIN	O29443 salmo salar
28	35	53.8	895	1 GND6_RAT	O13967 homo sapien
29	35	53.8	914	1 GND6_HUMAN	O13967 homo sapien
30	35	53.8	1333	1 PAD3_MOUSE	O95h2 mus musculu
31	35	53.8	1337	1 PAD3_RAT	O95h2 mus musculu
32	35	53.8	2663	1 CENE_HUMAN	O02224 homo sapien
33	34	52.3	81	1 YC54_PASNU	O9c6g4 pasteurilla

34	34	52.3	125	1 YBJM_ECOLI	P75813 escherichia
35	34	52.3	239	1 6PGL_XYRFA	O9peg5 xylella fas
36	34	52.3	239	1 6PGL_XYRFT	O87eg7 xylella fas
37	34	52.3	246	1 Y208_MENTA	O57651 methanococc
38	34	52.3	276	1 Y938_TREPA	O83908 treponema p
39	34	52.3	294	1 MENA_MYCLE	O07134 mycobacteri
40	34	52.3	371	1 YB2X_HABIN	O86233 haemophilus
41	34	52.3	442	1 INSG_ECOLI	P03835 escherichia
42	34	52.3	499	1 CPML_ONCMY	O92088 oncorhynch
43	34	52.3	685	1 TRFE_PAROL	O93429 paratubercu
44	34	52.3	771	1 KIR1_VACCC	P20503 vaccinia vi
45	34	52.3	771	1 KIR1_VACCV	P12848 vaccinia vi

ALIGNMENTS

RESULT 1	TRFL_BUBBU	STANDARD;	PRT;	708 AA.
ID	TRFL_BUBBU			
AC	O77698:			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Lactotransferrin precursor (Lactoterrin).			
GN	LTF.			
OS	Bubalus bubalis (Domestic water buffalo).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bubalus.			
OX	NCBI_TaxID=89462;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Paramesivam M., Thatraliyath B.D., Kumar A., Srinivasan A.,			
RA	Singh T.P.;			
RT	"CDNA sequence of Buffalo lactoferrin."			
RT	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
RL	(2)			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).			
RX	MEDLINE=20003130; PubMed=10531476;			
RA	Karthikeyan S., Paramesivam M., Yadav S., Srinivasan A., Singh T.P.;			
RT	"Structure of buffalo lactoferrin at 2.5-A resolution using crystals			
RT	grown at 303 K shows different orientations of the N and C lobes."			
RL	Acta Crystallogr. D 55:1805-1813 (1999).			
CC	- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH			
CC	CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING			
CC	OF AN ANION, USUALLY BICARBONATE.			
CC	- SUBUNIT: Monomer.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- DOMAIN: Composed of two homologous domains.			
CC	- SIMILARITY: Belongs to the transferrin family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collabora-			
CC	tion between the Swiss Institute of Bioinformatics and the EMBL outstation-			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AJ005203; CA06441.1; -			
DR	PDB; 1CE2; 13-MAR-99.			
DR	PDB; 1B1Y; 13-JAN-99.			
DR	InterPro; IPR001156; Transferrin.			
DR	Pfam; PF00405; Transferrin; 2.			
DR	PRINTS; PR00422; TRANSFERIN.			
DR	SMART; SM00094; TR_FER; 2.			
DR	PROSITE; PS00205; TRANSFERRIN_1; 2.			
DR	PROSITE; PS00206; TRANSFERRIN_2; 2.			
DR	PROSITE; PS00207; TRANSFERRIN_3; 2.			
KW	Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;			
KW	Signal; 3d-structure.			
FT	SIGNAL			
FT	1			
FT	19			

FT	CHAIN	20	708	LACTOTRANSFERIN.
FT	DISULFID	28	64	
FT	DISULFID	38	55	
FT	DISULFID	134	217	
FT	DISULFID	176	192	
FT	DISULFID	179	202	
FT	DISULFID	189	200	
FT	DISULFID	250	264	
FT	DISULFID	367	399	
FT	DISULFID	377	390	
FT	DISULFID	424	703	
FT	DISULFID	444	666	
FT	DISULFID	476	551	
FT	DISULFID	500	694	
FT	DISULFID	510	524	
FT	DISULFID	521	534	
FT	DISULFID	592	606	
FT	DISULFID	644	649	
FT	METAL	79	79	IRON 1.
FT	METAL	111	111	IRON 1.
FT	METAL	211	211	IRON 1.
FT	METAL	272	272	IRON 1.
FT	METAL	414	414	IRON 2.
FT	METAL	452	452	IRON 2.
FT	METAL	545	545	IRON 2.
FT	METAL	614	614	IRON 2.
FT	BINDING	136	136	CARBONATE 1.
FT	BINDING	140	140	CARBONATE 1.
FT	BINDING	142	142	CARBONATE 1 (VIA AMIDE NITROGEN).
FT	BINDING	143	143	CARBONATE 1 (VIA AMIDE NITROGEN).
FT	BINDING	478	478	CARBONATE 2.
FT	BINDING	482	482	CARBONATE 2.
FT	BINDING	484	484	CARBONATE 2 (VIA AMIDE NITROGEN).
FT	BINDING	485	485	CARBONATE 2 (VIA AMIDE NITROGEN).
FT	CARBOHYD	252	252	N-LINKED (GLUCNAC. . .) (POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLUCNAC. . .) (POTENTIAL).
FT	CARBOHYD	495	495	N-LINKED (GLUCNAC. . .) (POTENTIAL).
FT	CARBOHYD	564	564	N-LINKED (GLUCNAC. . .) (POTENTIAL).
FT	TURN	21	22	
FT	STRAND	25	29	
FT	HELIX	32	46	
FT	TURN	47	48	
FT	STRAND	53	57	
FT	HELIX	61	69	
FT	TURN	70	71	
FT	STRAND	75	78	
FT	HELIX	80	87	
FT	TURN	89	91	
FT	STRAND	93	102	
FT	STRAND	107	108	
FT	STRAND	110	118	
FT	TURN	119	120	
FT	HELIX	125	127	
FT	TURN	129	130	
FT	STRAND	132	135	
FT	TURN	138	139	
FT	TURN	141	144	
FT	HELIX	145	150	
FT	TURN	151	151	
FT	HELIX	152	155	
FT	TURN	159	161	
FT	HELIX	164	169	
FT	TURN	170	171	
FT	STRAND	174	176	
FT	TURN	178	179	
FT	TURN	182	184	
FT	HELIX	186	189	
FT	TURN	190	191	
FT	HELIX	196	198	
FT	TURN	199	200	
FT	TURN	204	205	
FT	TURN	207	208	
FT	HELIX	211	219	

Query Match 100.0%; Score 65; DB 1; Length 708;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ARARVWCAGV 12
 |||||
 359 ARARVWCAGV 370

RESULT 2
 TRFL_HUMAN STANDARD; PRT; 711 AA.
 ID TRFL_HUMAN Q16780; Q16780; Q16785; Q16789; Q96K24; Q96K25;
 AC P02788; C00756; Q16780; Q16785; Q16789; Q96K24; Q96K25;
 AC Q9H123; 1986 (Rel. 01; Created)
 DT 21-JUL-1986 (Rel. 01; Created)
 DT 15-JUL-1999 (Rel. 38; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A;
 DE Lactoferrin B; Lactoferrin C].
 GN LTF OR LF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 NX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=90384839; PubMed=240245;
 RT "Rey M.W., Woloshuk S.U., de Boer H.A., Pieper F.R.;
 RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
 RL Nucleic Acids Res. 18:5288-5288(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX Cno Y.Y.;
 RT Thesis (1994), Genetic Engineering Research Institute / Taejeon, Korea.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Connolly O.M.;
 RT Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX Liang Q., Jimenez-Plores R., Richardson T.;
 RT "Molecular cloning and sequence analysis of human lactoferrin.";
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX Wei X., Han J., Rado T.A.;
 RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
 RT sequences.";
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX Cheng H., Chen X., Huan L.;
 RT "cDNA cloning and sequence analysis of human lactoferrin.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=2238257; PubMed=12477932;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Murnusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stetson M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carrincci P., Prange S.J.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Bakerley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 3-711 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=90326549; PubMed=2374734;
 RA Powell M.J., Ogden J.E.;
 RT "Nucleotide sequence of human lactoferrin cDNA.";
 RL Nucleic Acids Res. 18:4013-4013(1990).
 RN [9]
 RP SEQUENCE OF 20-711.
 RX MEDLINE=8507667; PubMed=6510420;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoengen F.,
 RA Legendre D., Spik G., Montreuil J., Jolles P.;
 RT "Human lactoferrin: amino acid sequence and structural
 RT comparisons with other transferrins.";
 RL Eur. J. Biochem. 145:659-666(1984).
 RN [10]
 RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
 RX MEDLINE=8204617; PubMed=6794640;
 RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
 RA Jolles P.;
 RT "The present state of the human lactoferrin sequence. Study and
 RT alignment of the cyanogen bromide fragments and characterization of
 RT N- and C-terminal domains.";
 RL Biochim. Biophys. Acta 670:243-254(1981).
 RN [11]
 RP SEQUENCE OF 609-711.
 RX MEDLINE=82262043; PubMed=7049727;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
 RA Jolles P.;
 RT "An 88 amino acid long C-terminal sequence of human
 RT lactoferrin.";
 RL FEBS Lett. 142:107-110(1982).
 RN [12]
 RP SEQUENCE OF 436-711 FROM N.A.
 RX MEDLINE=88001031; PubMed=3477300;
 RA Rado T.A., Wei X., Benz E.J. Jr.;
 RT "Isolation of lactoferrin cDNA from a human myeloid library and
 RT expression of mRNA during normal and leukemic myelopoiesis.";
 RL Blood 70:989-993(1987).
 RN [13]
 RP SEQUENCE OF 237-711 FROM N.A.
 RA McComb W.R., Wilson R., Chen E., Gibbs R., Zhu L., Johnson D.,
 RA Nhan M., Parnell L., Dedina N., Ansari A., Mardis E., Schütz K.,
 RA Gao J., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
 RA Sagripanti J.L.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
 RX MEDLINE=90064528; PubMed=2585506;
 RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
 RT "Structure of human lactoferrin: crystallographic structure analysis
 RT and refinement at 2.8 Å resolution.";
 RL J. Mol. Biol. 209:711-734(1989).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RA Hardias M., Anderson B.F., Baker E.N.;
 RT "Structure of human diferric lactoferrin refined at 2.2 Å
 RT resolution.";
 RL Acta Crystallogr. D 51:629-646(1995).

RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
 RX MEDLINE=97156796; PubMed=9003186;
 RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
 Baker E.N.;
 RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
 binding properties and crystal structure of the histidine-
 RT 253->methionine mutant."
 RL Biochemistry 36:341-346(1997).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=99190892; PubMed=10089347;
 RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
 RT "Structure of recombinant human lactoferrin expressed in Aspergillus
 RT awamori."
 RL Acta Crystallogr. D 55:403-407(1999).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99192677; PubMed=10089508;
 RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
 RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
 RT and analysis of ligand-induced conformational change."
 RL Acta Crystallogr. D 54:1319-1335(1998).
 RN [19]
 RP CHARACTERIZATION OF LACTOFERROXINS.
 RX MEDLINE=9116929; PubMed=1369293;
 RA Tani F., Ito K., Chiba H., Yoshikawa M.;
 RT "Isolation and characterization of opioic antagonist peptides derived
 RT from human lactoferrin."
 RL Agric. Biol. Chem. 54:1803-1810(1990).
 RN [20]
 RP VARIANTS THR-30 AND ARG-48.
 RX MEDLINE=99091914; PubMed=9873069;
 RA Klimworth G.K., Sommer J.R., O'Brien G., Han L., Ahmed M.N.,
 RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
 RA Sagar J., Kumaramanickavel G., Muller F., Schorderet D.F.,
 RA El Metri L., Inata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
 RA Hightanck U.F., Teng C.T.;
 RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
 RT corneal dystrophy): exclusion of linkage to lactoferrin gene."
 RL Mol. Vision 4:11-32(1998).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
 CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
 CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
 CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 DR EMBL; X53961; CAA37914.1; -;
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 DR EMBL; M93150; AAA36159.1; -;
 DR EMBL; M83202; AAA59511.1; -;
 DR EMBL; M83205; AAA58656.1; -;
 Query Match 100.0%; Score 65; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 12; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AARAVWCavg 12
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DB 360 AARAVWCavg 371
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 AC 07811.
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Saliv;
 RX MEDLINE=99296631; PubMed=10366507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare dimeric lactoferrin at 2.6-A
 RT resolution."
 RL J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 DR EMBL; AJ010930; CAA09407.1; -;
 DR PDB; 1B1X; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR PDB; 1F93; 10-FEB-01.
 DR PDB; 11EB; 13-FEB-02.
 DR PDB; 1QW; 14-JAN-00.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 KM Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3D-structure.
 FT NON TER 1 1
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DT 01-APR-1990 (Rel. 14, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NX NCBI_TaxID=9823;
 RP [1].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92379101; PubMed=1511016;
 RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Heaton D.R.,
 RA Comeely O.M.;
 RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.",
 RL Biochim. Biophys. Acta 1132:97-99(1992).
 RP [2].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92367939; PubMed=1503259;
 RA Alexander L.J., Levine W.B., Teng C.T., Beattie C.W.;
 RT "Cloning and sequencing of the porcine lactoferrin cDNA.",
 RL Anim. Genet. 23:251-256(1992).
 RP [3].
 RP SEQUENCE OF 20-49.
 RX MEDLINE=90105538; PubMed=2605266;
 RA Hutchens T.W., Magnuson J.S., Yip T.-T.;
 RT "Rapid purification of porcine colostrum whey lactoferrin by affinity
 RT chromatography on single-stranded DNA-agarose. Characterization,
 RT amino acid composition and N-terminal amino acid sequence.",
 RL Biochim. Biophys. Acta 989:323-329(1989).
 CC - FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC - SUBUNIT: Monomer.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - DOMAIN: Composed of two homologous domains.
 CC - SIMILARITY: Belongs to the transferrin family.
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 CC -----
 DR EMBL: M92089; AAA31102.1; -
 DR EMBL: M81327; AAA31059.1; -
 DR PIR: A45543; A45543.
 DR HSSP: 07698; 1CE2.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN 1; 2.
 DR PROSITE: PS00206; TRANSFERRIN 2; 2.
 DR PROSITE: PS00207; TRANSFERRIN 3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 704 LACTOTRANSFERRIN.
 FT REPEAT 20 359 1.
 FT REPEAT 360 704 2.
 FT DISULFID 28 62 BY SIMILARITY.
 FT DISULFID 38 53 BY SIMILARITY.
 FT DISULFID 130 213 BY SIMILARITY.
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 FT DISULFID 246 260 BY SIMILARITY.
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 FT DISULFID 472 547 BY SIMILARITY.

FT DISULFID 496 690 BY SIMILARITY.
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 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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 Db 355 ARQAKVWCAVG 366
 TRFL CAMDR STANDARD; PRT; 708 AA.
 AC 09TUM0; 09WZ55;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NX NCBI_TaxID=9838;
 RP [1].
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Pahan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.",
 RL Int. Dairy J. 9:481-486(1995).
 RP [2].
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
- SUBUNIT: Monomer (BY SIMILARITY).
- SUBCELLULAR LOCATION: Secreted.
- DOMAIN: Composed of two homologous domains.
- SIMILARITY: Belongs to the transferrin family.

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CC EMBL; AJ131674; CAB53387.1; -
CC EMBL; AF165879; AAF82241.1; -
CC PDB; 1DTZ; 20-JUN-01; -
CC InterPro; IPR001156; "transferrin".
CC Pfam; PF00405; "transferrin"; 2.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transports; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3d-structure.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IROIN 1 (BY SIMILARITY).
FT METAL 111 111 IROIN 1 (BY SIMILARITY).
FT METAL 211 211 IROIN 1 (BY SIMILARITY).
FT METAL 272 272 IROIN 2 (BY SIMILARITY).
FT METAL 414 414 IROIN 2 (BY SIMILARITY).
FT METAL 452 452 IROIN 2 (BY SIMILARITY).
FT METAL 545 545 IROIN 2 (BY SIMILARITY).
FT METAL 614 614 CARBONATE 1 (BY SIMILARITY).
FT METAL 614 136 CARBONATE 1 (BY SIMILARITY).
FT METAL 140 140 CARBONATE 1 (BY SIMILARITY).
FT METAL 142 142 CARBONATE 1 (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 484 484 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 485 485 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MW; 0B0C175A0B59D430 CRC64;
Query Match 87.7%; Score 57; DB 1; Length 708;
Best Local Similarity 90.9%; Pred. No. 0.0086;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 2 RRAVWCAVG 12
Db 360 RRAQVWCAVG 370
RESULT 6
TFPL_BOVIN STANDARD; PRT; 708 AA.
AC P24627; Q29629; Q9MWX3;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [contains: Lactoferricin B
(LFCIN B)].
GN LTF
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=Submaxillary gland;
RC MEDLINE=91160501; PubMed=2001696;
RX Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
RA Montreuil J., Spik G.;
RT "Molecular cloning and sequence analysis of bovine lactotransferrin";
RL Eur. J. Biochem. 196;177-184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92028986; PubMed=1718281;
RX Goodman R.E., Schanbacher F.L.;
RA "Bovine lactoferrin mRNA: sequence, analysis, and expression in the
RT mammary gland.";
RL Biochem. Biophys. Res. Commun. 180:75-84(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Tsang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;
RA "Cloning of a 80-kD advanced glycosylation end product (AGE) binding
RT protein from bovine lung";
RL FASEB J. 6:233-233(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Mammary gland;
RX MEDLINE=9426164; PubMed=8206385;
RX Seyfert H.-M., Tuckovic A., Interthal H., Koczan D., Hobom G.;
RA "Structure of the bovine lactoferrin-encoding gene and its promoter";
RL Gene 143:265-269(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX Nakamura I., Shimazaki K., Yagi Y., Watanabe A.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 20-59.
RX MEDLINE=90031466; PubMed=2805645;
RX Rejman J.J., Hegarty H.M., Hurley W.L.;
RA "Purification and characterization of bovine lactoferrin from
RT secretions of the involuting mammary gland: identification of


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FT TURN 196 197
Query Match 83.1%; Score 54; DB 1; Length 708;
Best Local Similarity 83.3%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARBARYWCAVG 12
DB 359 ARTRYWCAVG 370

RESULT 7
TRFL_CAPHI STANDARD; PRT; 708 AA.
AC 029477; 029479; 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OC NCBI_TaxID=9925;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=94380047; PubMed=8093048;
RA le Provost F., Nocart M., Guerin G., Martin P.;
RT "Characterization of the goat lactoferrin cDNA. Assignment of the
RT relevant locus to bovine U12 syntenic group.";
RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION. USUALLY BICARBONATE.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC
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CC
CC -----
CC EMBL: U53857; AAA97958.1; -
CC EMBL: X78902; CA55517.1; -
CC DR HSBP; 077698; ICE2.
CC DR InterPro; IPR001156; Transferrin.
CC DR Pfam; PF00405; Transferrin; 2.
CC DR PRINTS; PRO0422; TRANSFERRIN.
CC DR SMART; SM00094; TR_FER. 2.
CC DR PROSITE; PS00205; TRANSFERRIN 1; 2.
CC DR PROSITE; PS00206; TRANSFERRIN 2; 2.
CC DR PROSITE; PS00207; TRANSFERRIN 3; 2.
CC DR Transprot; Itron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal.
CC KW SIGNAL.
CC FT CHAIN 1 19 BY SIMILARITY.
CC FT REPEAT 20 708 LACTOTRANSFERRIN.
CC FT REPEAT 20 363 1.
CC FT REPEAT 364 708 2.
CC FT DISULFID 28 64 BY SIMILARITY.
CC FT DISULFID 38 55 BY SIMILARITY.
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FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 BY SIMILARITY.
FT METAL 111 111 BY SIMILARITY.
FT METAL 211 211 BY SIMILARITY.
FT METAL 272 272 BY SIMILARITY.
FT METAL 414 414 BY SIMILARITY.
FT METAL 452 452 BY SIMILARITY.
FT METAL 545 545 BY SIMILARITY.
FT METAL 614 614 BY SIMILARITY.
FT BINDING 140 140 BY SIMILARITY.
FT BINDING 142 142 BY SIMILARITY.
FT BINDING 143 143 BY SIMILARITY.
FT BINDING 478 478 BY SIMILARITY.
FT BINDING 482 482 BY SIMILARITY.
FT BINDING 484 484 BY SIMILARITY.
FT BINDING 485 485 BY SIMILARITY.
FT CARBOHYD 252 252 BY SIMILARITY.
FT CARBOHYD 300 300 BY SIMILARITY.
FT CARBOHYD 387 387 BY SIMILARITY.
FT CARBOHYD 495 495 BY SIMILARITY.
FT CARBOHYD 564 564 BY SIMILARITY.
FT CONFLICT 56 56 BY SIMILARITY.
FT CONFLICT 88 88 BY SIMILARITY.
FT CONFLICT 124 124 BY SIMILARITY.
FT CONFLICT 154 154 BY SIMILARITY.
FT CONFLICT 304 304 BY SIMILARITY.
FT CONFLICT 414 414 BY SIMILARITY.
SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C853960D CMC64;

Query Match 81.5%; Score 53; DB 1; Length 708;
Best Local Similarity 83.3%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARBARYWCAVG 12
DB 359 ARTRYWCAVG 370

RESULT 8
TRFL_MOUSE STANDARD; PRT; 707 AA.
AC P08071; P70690; Q61799; Q922P2;
DT 01-AUG-1988 (Rel. 08, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN LTF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=87280033; PubMed=36.1056;
RA Pentecost B.T., Teng C.T.;
RT "The major estrogen-inducible protein of mouse
```

uterine secretions.";
J. Biol. Chem. 262:10134-10139 (1987).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Morishi K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijy S.W.,
Vallion D.K., Muzny D.M., Halse S., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
Schererch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[4]
SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=92042099; PubMed=19392212;
RA Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885 (1991).
- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
- SUBUNIT: Monomer.
- SUBCELLULAR LOCATION: Secreted.
- DOMAIN: Composed of two homologous domains.
- SIMILARITY: Belongs to the transferrin family.
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DR EMBL: J03298; AAA40525.1; -
DR EMBL: D88510; BAA13633.1; -
DR EMBL: BC006904; AAH06904.1; -
DR EMBL: M74778; AAA39427.1; -
DR HSSP: P02788; 1CB6;
DR MGD; MGI:96837; LfE;
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transferrin; Iron transport; Glycoprotein; Metal binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 707 707 LACTOTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 707 2.
FT DISULFID 27 63 BY SIMILARITY.
FT DISULFID 37 54 BY SIMILARITY.

FT DISULFID 133 216 BY SIMILARITY.
FT DISULFID 175 191 BY SIMILARITY.
FT DISULFID 188 199 BY SIMILARITY.
FT DISULFID 249 263 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 702 BY SIMILARITY.
FT DISULFID 443 665 BY SIMILARITY.
FT DISULFID 475 550 BY SIMILARITY.
FT DISULFID 499 693 BY SIMILARITY.
FT DISULFID 509 523 BY SIMILARITY.
FT DISULFID 520 533 BY SIMILARITY.
FT DISULFID 591 605 BY SIMILARITY.
FT DISULFID 643 648 BY SIMILARITY.
FT METAL 78 78 IRON 1 (BY SIMILARITY).
FT METAL 110 110 IRON 1 (BY SIMILARITY).
FT METAL 210 210 IRON 1 (BY SIMILARITY).
FT METAL 271 271 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 451 451 IRON 2 (BY SIMILARITY).
FT METAL 454 544 IRON 2 (BY SIMILARITY).
FT METAL 613 613 IRON 2 (BY SIMILARITY).
FT BINDING 135 135 CARBONATE 1 (BY SIMILARITY).
FT BINDING 139 139 CARBONATE 1 (BY SIMILARITY).
FT BINDING 141 141 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 477 477 CARBONATE 2 (BY SIMILARITY).
FT BINDING 481 481 CARBONATE 2 (BY SIMILARITY).
FT BINDING 483 483 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 484 484 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1 2 MR -> IQG (IN REF. 1).
FT CONFLICT 25 25 R -> Q (IN REF. 2).
FT CONFLICT 82 82 M -> L (IN REF. 2).
FT CONFLICT 359 359 S -> T (IN REF. 2).
FT CONFLICT 382 382 A -> D (IN REF. 1).
FT CONFLICT 449 449 E -> G (IN REF. 2).
FT CONFLICT 629 629 L -> V (IN REF. 1).
SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;
Query Match 80.0%; Score 52; DB 1; Length 707;
Best Local Similarity 75.0%; Pred. No. 0.07;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 ARRAVTCVAVG 12
Db 358 ASKARVTCVAVG 369

RESULT 9
ICA_PIG STANDARD; PRT; 704 AA.
AC Q29545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inhibitor of carbonic anhydrase precursor.
GN ICA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97254619; PubMed=9100029;
RA Wiebels M.W., Roush E.D., Decastro C.M., Fierke C.A.;
"Cloning, sequencing, and recombinant expression of the porcine
inhibitor of carbonic anhydrase: a novel member of the transferrin

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RT family";
RL Biochemistry 36:4327-4336(1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93099129; PubMed=1463741;
RA Roush E.D., Fleerke C.A.;
RT "Purification and characterization of a carbonic anhydrase II
RL inhibitor from porcine plasma.";
RT Biochemistry 31:12536-12542(1992).
CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
CC with nanomolar affinity.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PFM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the transferrin family.
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DR EMBL; U36916; AAB58956.1; -.
DR PIR; I47228; I47228.
DR HSSP; P19134; ITPD.
DR InterPro: IPR001156; Transferrin.
DR Pfam: PF00405; TRANSFERRIN_2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
DR KMW Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 704
FT CARBOHYD 491 491
FT SEQUENCE 704 AA; 77634 MW; 16B80E651931E336 CRC64;
SQ
Query Match 67.7%; Score 44; DB 1; Length 704;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 RYVWCAGV 12
Db 356 RYVWCAGV 363
RESULT 10
ID TREE_CHICK STANDARD; PRT; 705 AA.
AC P02789;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovocytotransferrin precursor (Conalbumin) (Allergen Gal d 3) (Gal d III)
DE (Serum transferrin).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82138851; PubMed=7060577;
RA Jeltsch J.-M., Chambon P.;
RT "The complete nucleotide sequence of the chicken ovotransferrin
RT mRNA.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428516; PubMed=10497206;
RA Kurokawa H., Dewan J.C., Mikami B., Sacchetti J.C., Hirose M.;

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FT METAL 450 450 IRON 2.
FT METAL 543 543 IRON 2.
FT METAL 611 611 IRON 2.
FT BINDING 136 136 CARBONATE 1.
FT BINDING 140 140 CARBONATE 1.
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN).
FT BINDING 475 475 CARBONATE 2.
FT BINDING 479 479 CARBONATE 2.
FT BINDING 481 481 CARBONATE 2 (VIA AMIDE NITROGEN).
FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN).
FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .).
FT VARIANT 83 83 A -> V.
FT VARIANT 100 100 A -> I.
FT VARIANT 154 154 R -> W.
FT VARIANT 239 240 OK -> LN.
FT VARIANT 686 686 S -> N.
FT CONFLICT 132 132 T -> N (IN REF. 1).
FT CONFLICT 317 317 L -> F (IN REF. 1).
FT STRAND 25 30
FT HELIX 33 45
FT STRAND 52 57
FT HELIX 61 69
FT TURN 70 71
FT STRAND 75 78
FT HELIX 80 86
FT TURN 87 87
FT TURN 89 91
FT STRAND 94 100
FT STRAND 110 118
FT TURN 119 120
FT HELIX 125 127
FT TURN 129 130

Query Match 66.2%; Score 43; DB 1; Length 705;
Best Local Similarity 63.6%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0.

Qy 2 RRARVWCAGV 12
Db 360 RRRRIQWCAVG 370

RESULT 11
TRFE_ANAPL STANDARD; PRT; 686 AA.
ID TRFE_ANAPL P56410;
AC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovotransferrin.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
[1]
RN RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS).
RA Rawas A., Muirhead H., Williams J.;
RT "Structure of apo duck ovotransferrin: the structures of the N and C
RL Acta Crystallogr. D 53:464-468 (1997).
[2]
RN RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS).
RA Rawas A., Muirhead H., Williams J.;
RT "Structure of ferric duck ovotransferrin at 2.35-A resolution.";
RL Acta Crystallogr. D 52:631-640 (1996).
[2]
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -!- FUNCTION: OVOTRANSFERRIN HAS A BACTERIOSTATIC FUNCTION. ITS

```

CONCENTRATION IN AVIAN EGG IS THE HIGHEST CONCENTRATION OF ANY
TRANSFERIN IN VIVO (BY SIMILARITY).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
DR PDB; 1A0V; 16-JUN-97.
DR PDB; 1DOT; 08-MAR-96.
DR PDB; 1GV8; 03-MAY-02.
DR PDB; 1GVC; 03-MAY-02.
DR PDB; 1OVB; 31-JAN-94.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Transferrin; Iron transport; Glycoprotein; Metal-binding; Repeat;
3D-structure.
KW REPEAT 1 332 1.
FT DOMAIN 333 341 CONNECTING REGION.
FT REPEAT 342 686 2.
FT DISULFID 10 45
FT DISULFID 20 36
FT DISULFID 115 197
FT DISULFID 160 174
FT DISULFID 171 182
FT DISULFID 228 242
FT DISULFID 348 380
FT DISULFID 358 371
FT DISULFID 405 680
FT DISULFID 421 643
FT DISULFID 454 530
FT DISULFID 478 671
FT DISULFID 488 502
FT DISULFID 499 513
FT DISULFID 570 584
FT CARBOHYD 473 473
FT CARBOHYD 548 548
FT STRAND 6 11
FT TURN 14 15
FT HELIX 16 23
FT TURN 24 29
FT STRAND 33 38
FT STRAND 42 50
FT HELIX 51 53
FT TURN 55 59
FT STRAND 61 67
FT HELIX 68 68
FT TURN 70 71
FT TURN 75 81
FT STRAND 91 99
FT STRAND 100 101
FT TURN 106 108
FT HELIX 110 111
FT TURN 113 116
FT STRAND 122 125
FT TURN 126 135
FT HELIX 132 135
FT HELIX 152 155
FT STRAND 158 160
FT TURN 162 163
FT TURN 169 173
FT TURN 181 182
FT TURN 187 188
FT TURN 190 200
FT HELIX 201 201
FT TURN 205 209
FT STRAND 210 211
FT TURN 212 216
FT HELIX 221 223
FT STRAND 224 228
FT TURN 229 231

N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT STRAND 232 235
FT TURN 236 237
FT STRAND 245 248
FT STRAND 251 254
FT HELIX 260 274
FT HELIX 293 295
FT TURN 302 303
FT STRAND 306 309
FT TURN 312 313
FT HELIX 316 320
FT STRAND 323 332
FT HELIX 342 343
FT STRAND 345 350
FT HELIX 352 365
FT TURN 366 366
FT STRAND 369 374
FT HELIX 378 385
FT TURN 386 387
FT STRAND 391 394
FT HELIX 396 403
FT TURN 404 406
FT STRAND 408 414
FT TURN 417 418
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FT HELIX 465 475
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FT HELIX 534 534
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FT HELIX 545 548
FT TURN 557 559
FT HELIX 563 565
FT STRAND 567 569
FT TURN 571 572
FT STRAND 575 577
FT TURN 578 579
FT TURN 582 583
FT STRAND 587 589
FT STRAND 593 596
FT TURN 598 600
FT HELIX 601 615
FT TURN 617 618
FT TURN 620 624
FT TURN 627 628
FT TURN 639 640
FT STRAND 643 646
FT TURN 649 650
FT HELIX 653 657
FT HELIX 659 668
FT TURN 669 670
FT HELIX 675 683
FT TURN 684 686
SQ SEQUENCE 686 AA; 75632 MW; 963FCF4727C3EBDD CRC64;

Query Match 61.5%; Score 40; DB 1; Length 686;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 RRARVWCavg 12

Db 341 RENKIMCAGV 351

RESULT 12

REP2_ECOLI STANDARD; PRT; 285 AA.
AC P03066; Q47411;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Replication initiation protein.
OS Escherichia coli.
OC Plasmid IncFII R100, Plasmid IncFII R1, and Plasmid IncFII NR1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII R100;
RX MEDLINE=81074309; PubMed=7003300;
RA Rosen J., Ryder T., Inokuchi H., Ohtsubo E.;
RT "Genes and sites involved in replication and incompatibility of an
RT R100 plasmid derivative based on nucleotide sequence analysis.";
RL Mol. Gen. Genet. 179:527-537(1980).
RN [2]
RP SEQUENCE OF 1-77 FROM N.A.
RC PLASMID=IncFII R100, and IncFII R1;
RX MEDLINE=81173118; PubMed=6163994;
RA Rosen J., Ryder T., Ohtsubo H., Ohtsubo E.;
RT "Role of RNA transcripts in replication incompatibility and copy
RT number control in antibiotic resistance plasmid derivatives.";
RL Nature 280:794-797(1981).
RN [3]
RP SEQUENCE OF 270-285 FROM N.A.
RC PLASMID=IncFII R1;
RX MEDLINE=88289416; PubMed=3041379;
RA Masai H., Arai K.;
RT "Repa protein- and oriR-dependent initiation of R1 plasmid
RT replication: identification of a rho-dependent transcription
RT terminator required for cis-action of repA protein.";
RL Nucleic Acids Res. 16:6493-6514(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII NR1;
RX MEDLINE=89011975; PubMed=3050127;
RA Dong X., Womble D.D., Rownd R.H.;
RT "In vivo studies on the cis-acting replication initiator protein of
RT IncFII plasmid NR1.";
RL J. Mol. Biol. 202:495-509(1988).
RN [5]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII NR1;
RX MEDLINE=85160860; PubMed=2580099;
RA Womble D.D., Sampathkumar P., Easton A.M., Luckow V.A., Rownd R.H.;
RT "Transcription of the replication control region of the IncFII
RT R-plasmid NR1 in vitro and in vivo.";
RL J. Mol. Biol. 181:395-410(1985).
RN [6]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII R100;
RX MEDLINE=86319522; PubMed=3019092;
RA Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;
RT "DNA replication of the resistance plasmid R100 and its control.";
RL Adv. Biophys. 21:115-133(1986).
CC -1- FUNCTION: This protein is essential for plasmid replication; it is
CC involved in copy control functions.
CC -1- SIMILARITY: BELONGS TO THE INCFII REPA FAMILY.
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).

CC -----
CC DR EMBL; J01762; AAA92257.1; -
CC DR EMBL; J01770; -; NOT ANNOTATED_CDS.
CC DR EMBL; X12587; CAA31100.1; -
CC DR EMBL; X12776; CAA31263.1; -
CC DR EMBL; X02302; CAA26168.1; -
CC DR EMBL; X02302; CAA26169.1; -; ALT_INIT.
CC DR EMBL; M26840; AAA26067.1; -
CC DR PIR; A03602; IDECRP.
CC DR PIR; I64780; I64780.
CC DR InterPro; IPR003446; RepIcn.
CC DR Pfam; PF02387; IncFII repA; 1.
CC KW Plasmid; DNA replication; Plasmid copy control.
CC FT CONFLICT 55 R -> H (IN REF. 6).
CC SQ SEQUENCE 285 AA; 32755 MW; A21C9D59D24B26B CRC64;

Query Match 60.0%; Score 39; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRRVYV 8
Db 168 ARRRVYV 175

RESULT 13

CSX2_SCHPO STANDARD; PRT; 870 AA.
AC Q9U0E2; Q09425;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein csx2.
GN CSX2 OR SPBC1799.08C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
CX NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor A., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsi K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moulé S., Mungall K., Murphy L., Niblett D., Odeli C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicikert G., Aert R., Robben J., Grynolprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Filiz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mambut R., Purnelle B.,
RA Goffeau A., Cadieu E., Driano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Kochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forzberg S.L.,
RA Carattini L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Paulsen I., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).

[2]
 RN SEQUENCE OF 158-345 FROM N.A.
 RP Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
 RA Hirata A., Yanagida M.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 Art-GAP domain.
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 CC -----
 CC EMBL: AL109846; CAB52806.1; -
 CC EMBL: D83419; BA11920.1; -
 CC PIR: T39731; T39731.
 CC GenBank: SP086; SP086.1; -
 CC InterPro: IPR002110; ANK.
 CC InterPro: IPR001164; hrip_1like.
 CC InterPro: IPR001849; PH.
 CC Pfam: PF01412; ArtGap; 1.
 CC Pfam: PF00169; PH; 1.
 CC PRINTS: PR00405; REVINTACTING.
 CC SMART: SM00105; ArtGap; 1.
 CC SMART: SM00233; PH; 1.
 CC PROSITE: PS00115; ARFGAP; 1.
 CC PROSITE: PS00003; PH DOMAIN; 1.
 CC KEGG: K01003; Zinc-finger.
 CC FT DOMAIN 510 614 PH
 CC FT DOMAIN 670 791 ARF-GAP.
 CC FT ZN_FING 686 710 C4-TYPE.
 CC FT CONFLICT 158 166 NGSSPLYLC -> VVGQVLNMQ (IN REF. 2).
 CC SO SEQUENCE 870 AA; 99081 MW; 4B3ED6F6162E80C6 CRC64;
 CC -----
 CC Query Match 58.5%; Score 38; DB 1; Length 870;
 CC Best Local Similarity 75.0%; Pred. No. 30;
 CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC Cy 4 ARVWCAGV 11
 CC |||||
 CC Db 693 ARVWCAGV 700
 CC -----
 CC RESULT 14
 CC YH92_AERPE STANDARD; PRT; 176 AA.
 CC ID YH92_AERPE
 CC AC OYB03
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Hypothetical protein APE1792.
 CC GN APE1792.
 CC OS Aeropyrum pernix.
 CC OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 CC CC Desulfurococcales; Aeropyrum.
 CC CX NCBI_TaxID=56636;
 CC RX STRAIN=K1;
 CC RA MEDLINE=93310339; PubMed=10382966;
 CC RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 CC Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka H., Kosugi H.,
 CC Hasegawa A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 CC Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 CC Yamazaki J., Kusuda N., Oguchi A., Aoki K.-I., Kubota K.,
 CC Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 CC "Complete genome sequence of an aerobic hyper-thermophilic
 CC Crenarchaeon, Aeropyrum pernix K1";
 CC RL DNA Res. 6:83-101(1999).
 CC -1- SIMILARITY: Belongs to the UPF0097 family.

CC -----
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 CC -----
 CC EMBL: AP000062; BA80795.1; -
 CC PIR: F72563; F72563.
 CC InterPro: IPR004175; 2.5_ligase.
 CC Pfam: PF02834; 2.5_ligase; 2.
 CC KEGG: K01003; Complete proteome.
 CC SO SEQUENCE 176 AA; 19666 MW; C8BD5FC929F7E56D CRC64;
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 CC Query Match 56.9%; Score 37; DB 1; Length 176;
 CC Best Local Similarity 70.0%; Pred. No. 9.8;
 CC Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC -----
 CC Cy 3 RARVWCAGV 12
 CC |||||
 CC Db 72 RARVWCAGV 81
 CC -----
 CC RESULT 15
 CC TRPE_HORSE STANDARD; PRT; 706 AA.
 CC ID TRPE_HORSE
 CC AC P27425
 CC DT 01-AUG-1992 (Rel. 23, Created)
 CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Serotransferrin precursor (Transferrin) (Beta-1-metal
 CC binding globulin).
 CC TF.
 CC GN Equus caballus (Horse).
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CC NCBI_TaxID=9796;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC MEDLINE=93277958; PubMed=8504171;
 CC Carpenter M.A., Broad T.E.;
 CC "The cDNA sequence of horse transferrin";
 CC Biochim. Biophys. Acta 1173:230-232(1993).
 CC [2]
 CC RP SEQUENCE FROM N.A.
 CC TISSUE=Extraembryonic tissue;
 CC RA McDowell K.J., Adams M.H., Baker C.B.;
 CC Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation to
 CC those of storage and utilization. Serum transferrin may also have
 CC a further role in stimulating cell proliferation.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 CC EMBL: M69020; AAA0958.1; -
 CC EMBL: U21127; AAA63684.1; -
 CC PIR: S33761; S33761.

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DR HSP; P02787; 1ABE.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN 1; 2.
DR PROSITE; PS00206; TRANSFERRIN 2; 2.
DR PROSITE; PS00207; TRANSFERRIN 3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 706 SEROTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 706 2.
FT DISULFID 26 64 BY SIMILARITY.
FT DISULFID 36 55 BY SIMILARITY.
FT DISULFID 134 215 BY SIMILARITY.
FT DISULFID 174 190 BY SIMILARITY.
FT DISULFID 177 198 BY SIMILARITY.
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FT DISULFID 498 692 BY SIMILARITY.
FT DISULFID 508 522 BY SIMILARITY.
FT DISULFID 519 533 BY SIMILARITY.
FT DISULFID 590 604 BY SIMILARITY.
FT DISULFID 642 647 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 209 209 IRON 1 (BY SIMILARITY).
FT METAL 270 270 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 449 449 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 612 612 IRON 2 (BY SIMILARITY).
FT BINDING 136 136 CARBONATE 1 (BY SIMILARITY).
FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 476 476 CARBONATE 2 (BY SIMILARITY).
FT BINDING 480 480 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 483 483 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT CARBOHYD 515 515 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 706 AA; 78094 MW; 1A0FA566C0409D8A CRC64;

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Query Match          56.9%; Score 37; DB 1; Length 706;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 5 RYVWCavg 12
Db 362 KYMCAIG 369

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Search completed: September 1, 2004, 00:10:41
Job time : 6.24667 secs

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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:56:54 ; Search time 22.24 Seconds
(without alignments)

170.244 Million cell updates/sec

Title: US-09-508-095-14

Sequence: 1 ARRARIWCAVG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	711	4	Q8TCD2
2	65	100.0	711	4	Q8TCD2
3	65	100.0	711	4	Q8TCD2
4	58	89.2	704	6	Q8TCD2
5	58	89.2	704	6	Q8TCD2
6	54	83.1	112	6	Q8TCD2
7	54	83.1	355	6	Q8TCD2
8	52	80.0	707	11	Q8TCD2
9	46	70.8	615	5	Q8TCD2
10	41	63.1	345	2	Q8TCD2
11	41	63.1	421	11	Q8TCD2
12	41	63.1	700	11	Q8TCD2
13	41	63.1	700	11	Q8TCD2
14	41	63.1	700	11	Q8TCD2
15	40	61.5	113	12	Q8TCD2
16	40	61.5	228	16	Q8TCD2

17	40	61.5	228	16	Q8TCD2
18	40	61.5	228	16	Q8TCD2
19	40	61.5	228	16	Q8TCD2
20	40	61.5	228	16	Q8TCD2
21	40	61.5	228	16	Q8TCD2
22	40	61.5	228	16	Q8TCD2
23	40	61.5	228	16	Q8TCD2
24	40	61.5	228	16	Q8TCD2
25	39.5	60.8	129	10	Q8TCD2
26	39	60.0	291	10	Q8TCD2
27	39	60.0	350	16	Q8TCD2
28	39	60.0	453	2	Q8TCD2
29	39	60.0	491	2	Q8TCD2
30	39	60.0	514	16	Q8TCD2
31	39	60.0	650	5	Q8TCD2
32	38	58.5	126	16	Q8TCD2
33	38	58.5	132	17	Q8TCD2
34	38	58.5	139	16	Q8TCD2
35	38	58.5	150	17	Q8TCD2
36	38	58.5	234	4	Q8TCD2
37	38	58.5	277	17	Q8TCD2
38	38	58.5	292	16	Q8TCD2
39	38	58.5	322	16	Q8TCD2
40	38	58.5	330	16	Q8TCD2
41	38	58.5	330	16	Q8TCD2
42	38	58.5	337	16	Q8TCD2
43	38	58.5	383	16	Q8TCD2
44	38	58.5	383	16	Q8TCD2
45	38	58.5	395	16	Q8TCD2

ALIGNMENTS

RESULT 1
Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAUSBERG R.;
RC TISSUE=Prostate;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
DR EMBL; BC022347; AAH22347.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; P:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion homeostasis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Iron transport; Metal-binding; Transport.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7E097045FAF CRC64;
Query Match 100.0%; Score 65; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0049;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 DB 360 ARARVWCAVG 371

RESULT 2

Q81ZHE PRELIMINARY; PRT; 711 AA.

AC Q81ZHE;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lactoferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kaplan J.B., Fine D.H.;
 RT "Characterization of an amino acid polymorphism in the antibacterial
 RT domain of human lactoferrin."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY137470; AN11304.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 SQ SEQUENCE 711 AA; 78396 MW; 547AB9423C27C67 CRC64;

Query Match 100.0%; Score 65; DB 4; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 DB 360 ARARVWCAVG 371

RESULT 3

Q81U92 PRELIMINARY; PRT; 711 AA.

AC Q81U92;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Shi Y.-Q., Zhang Y., Zheng Y.-M.;
 RT "Homo sapiens lactotransferrin Gene: cDNA Cloning and Sequence
 RT Analysis."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Tissue-Seminal vesicle;
 RC Baskar Singh S., Saravanan K., Paramasivam M., Srinivasan A.,
 RA Singh T.P.;

RT "Homo sapiens lactoferrin (HLF) mRNA."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY165046; AN63998.1; -
 DR EMBL; AY178998; AN75578.2; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006826; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KW Signal.
 FT SIGNAL.
 FT CHAIN
 SQ SEQUENCE 711 AA; 78382 MW; 547BFC42C9267867 CRC64;

Query Match 100.0%; Score 65; DB 4; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 DB 360 ARARVWCAVG 371

RESULT 4

Q8WNN8 PRELIMINARY; PRT; 704 AA.

AC Q8WNN8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Lactoferrin (Fragment).
 GN LTF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Wang S.-R., Lin T.-Y., Meng C.-N.;
 RT "Isolation and expression of porcine milk lactoferrin."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 DR EMBL; L77887; AA140161.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006826; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 KW Glycoprotein; Iron transport; Metal-binding; Transport.
 FT NON TER
 SQ SEQUENCE 704 AA; 77681 MW; 64EB769F7503CC32 CRC64;

Query Match 89.2%; Score 58; DB 6; Length 704;
 Best Local Similarity 83.3%; Pred. No. 0.079;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARPARVWCavg 12
 ||:|||||
 DB 355 ARQAKVWCavg 366

RESULT 5

Q7YS20 PRELIMINARY; PRT; 704 AA.
 ID Q7YS20
 AC 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lactoferrin.
 GN PLF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Pecorini C., Fogher C., Baldi A.;
 RT "The nucleotide sequence of porcine lactoferrin cDNA."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF306198; AAP70487.1; -
 SQ SEQUENCE 704 AA; 77522 MW; AAC8E1767E56BF6A CRC64;

Query Match

Best Local Similarity 83.3%; Score 58; DB 6; Length 704;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARPARVWCavg 12
 ||:|||||
 DB 355 ARQAKVWCavg 366

RESULT 6

Q9SM57 PRELIMINARY; PRT; 112 AA.
 ID Q9SM57
 AC Q9SM57
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-40 FROM N.A.
 RA Li G., Zhang Y., Li N.;
 RT "Analysis of the 5'-region of the bovine lactoferrin gene using PCR-
 SSCP."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY036583; AAK6816.1; -
 DR EMBL; AY036581; AAK6816.1; JOINED.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 FT NON_TER 1
 FT TER 112

QY 1 ARPARVWCavg 12
 ||:|||||
 DB 355 ARQAKVWCavg 366

Query Match 83.1%; Score 54; DB 6; Length 112;
 Best Local Similarity 83.3%; Pred. No. 0.076;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 66 ARYTRVWCavg 77
 ||:|||||

RESULT 7

Q8MT10 PRELIMINARY; PRT; 355 AA.
 ID Q8MT10
 AC Q8MT10
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lactotransferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 Montreuil J., Spik G.;
 RT "Molecular cloning and sequence analysis of bovine lactotransferrin."
 RL Eur. J. Biochem. 196; 177-184 (1991).
 DR EMBL; X17066; CAA34912.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 1.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR FER; 1.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 1.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 FT NON_TER 1
 FT TER 355

Query Match

Best Local Similarity 83.1%; Score 54; DB 6; Length 355;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARPARVWCavg 12
 ||:|||||
 DB 6 ARYTRVWCavg 17

RESULT 8

Q8CBA0 PRELIMINARY; PRT; 707 AA.
 ID Q8CBA0
 AC Q8CBA0
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lactotransferrin.
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RT Nature 420; 563-573 (2002).
 RL EMBL; AK036491; BAC29450.1; -
 DR MGD; MGI:96837; Ltf.
 DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008159; F:feric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMO0094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 707 AA; 77837 MW; EIB32FSD8748A0F CRC64;

Query Match 80.0%; Score 52; DB 11; Length 707;
Best Local Similarity 75.0%; Pred. No. 0.87;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRATVWCAVG 12
Db 358 ASKATVWCAVG 369

RESULT 9

Q9N906 PRELIMINARY; PRT; 615 AA.
AC Q9N906; 01-OCT-2000 (TREMUREL.15, Created)
DT 01-OCT-2000 (TREMUREL.15, Last sequence update)
DE 01-OCT-2003 (TREMUREL.25, Last annotation update)
DE Hypothetical protein.
GN L2464.09.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_Taxid=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin.
RA Brown S., Murphy L., Harris D., Ivens A.C., Quail M., Rajadream M.A.,
RA Barrell B.G.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin.
RX MEDLINE=9816435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.,
RT "A physical map of the Leishmania major Friedlin genome";
RL Genome Res. 8:135-145(1998);
DR EMBL; AJ365154; CAB96741.1; -;
DR GO; GO:0005759; Mitochondrial matrix; IEA.
DR InterPro; IPR003428; MAM33.
KW Hypothetical protein.
SQ SEQUENCE 615 AA; 67400 MW; A4AC2CCDB0F2DECB CRC64;

Query Match 70.8%; Score 46; DB 5; Length 615;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRATVWCA 10
Db 18 ARSRILWCA 27

RESULT 10
Q82HU3 PRELIMINARY; PRT; 254 AA.
AC Q82HU3; 01-JUN-2003 (TREMUREL.24, Created)
DT 01-JUN-2003 (TREMUREL.24, Last sequence update)
DE 01-OCT-2003 (TREMUREL.25, Last annotation update)
DE Putative short-chain dehydrogenase.
GN SAV3415.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=2147403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005035; BAC71127.1; -;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR002198; ADH_Short.
DR Pfam; PF00106; adh_Short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Complete proteome.
SQ SEQUENCE 254 AA; 26802 MW; 66CB807B046409F0 CRC64;

Query Match 63.1%; Score 41; DB 16; Length 254;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRATVWCA 10
Db 33 ARSRILWCA 42

RESULT 11
Q8KWB8 PRELIMINARY; PRT; 345 AA.
AC Q8KWB8; 01-OCT-2002 (TREMUREL.22, Created)
DT 01-OCT-2002 (TREMUREL.22, Last sequence update)
DE 01-JUN-2003 (TREMUREL.24, Last annotation update)
DE RB124.
OS Ruegeria sp. PR1b.
OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Ruegeria.
OX NCBI_Taxid=185586;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR1b;
RA Zhong Z., Toukarian A., Helinski D.R.,
RT "Characterization of two huge plasmids bearing marine bacteria
RT Ruegeria PR1b and sequence analysis.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416330; ZAN05145.1; -;
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
SQ SEQUENCE 345 AA; 38653 MW; AC9749D8E4FFD5E CRC64;

Query Match 63.1%; Score 41; DB 2; Length 345;
Best Local Similarity 63.6%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRATVWCAVG 12
Db 89 ORATVWCAVG 99

```
RESULT 12
Q7TPB3 PRELIMINARY; PRT; 421 AA.
ID Q7TPB3
AC Q7TPB3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aa2-001.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
RA Shi U.B., Rahman S., Wang Q.N., Zhang J.B.;
RT "Liver regeneration after PH.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY325160; AAP2561.1; -.
SQ SEQUENCE 421 AA; 46104 MW; F7FA084ABD73583A CRC64;

Query Match 63.1%; Score 41; DB 11; Length 421;
Best Local Similarity 87.5%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RVWCAVG 12
Db 81 RVWCAVG 88

RESULT 13
Q9BBD0 PRELIMINARY; PRT; 700 AA.
ID Q9BBD0
AC Q9BBD0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 130001702Rik protein.
GN 130001702Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=1217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
DR EMBL; AK005035; BAB23762.1; -.
DR HSSP; P19134; ITRF.
DR MGD; MGI:1919025; 130001702Rik.
DR GO; GO:0005576; C:extracellular; IEA.

RESULT 14
Q8VC96 PRELIMINARY; PRT; 700 AA.
ID Q8VC96
AC Q8VC96;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 1300017J02 gene.
GN 1300017J02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021390; AAH21390.1; -.
DR MGD; MGI:1919025; 130001702Rik.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; F:ferric iron binding; IEA.
DR GO; GO:0006826; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
SQ SEQUENCE 700 AA; 76795 MW; 7DA4A58CBB6BF37 CRC64;

Query Match 63.1%; Score 41; DB 11; Length 700;
Best Local Similarity 87.5%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RVWCAVG 12
Db 354 RVWCAVG 361

RESULT 15
O56754 PRELIMINARY; PRT; 113 AA.
ID O56754
AC O56754;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Non-structural protein 5 (genome polyprotein) (Fragment).
GN NS5.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
```

OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HC-P43;
 RX MEDLINE=98156956; PubMed=9497224;
 RA Wei L., Wang Y., Du S., Wang H., Tao Q.,
 RT "Genetic variability and characterization of non-structural region 5
 of hepatitis C virus genome from Chinese patients."
 RL J. Gastroenterol. 33:62-72(1998).
 DR EMBL; AF046203; AAC40552.1; -
 DR GO; GO:0019012; C:viral; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003668; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0016740; F:transcriptase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR InterPro; IPR002166; HCV_RdRp.
 DR InterPro; IPR007094; RNA_pol_PsVlr.
 DR Pfam; PF00998; Viral_RdRp_1_PsVlr.
 KW Nonstructural protein; Polypeptide; RNA-directed RNA polymerase;
 KM transferase.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12424 MW; 4DCP618FBCB8E87B CRC64;

QY 2 RRARVWCA 10
 Db 52 RRCVTWCS 60

Query Match 61.5%; Score 40; DB 12; Length 113;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Search completed: September 1, 2004, 00:15:30
 Job time : 26.24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:24 ; Search time 31.2867 Seconds
(without alignments)
117.402 Million cell updates/sec

Title: US-09-508-095-16

Perfect score: 70

Sequence: 1 AARARVWCAYGE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_29and04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	13	AAW93880	Aaw93880 Bifidobac
2	70	100.0	687	AAW71183	Aaw71183 Mutant hu
3	70	100.0	687	AAW71911	Aag77911 Human lac
4	70	100.0	688	AAW71182	Aaw71182 Mutant hu
5	70	100.0	688	AAW77910	Aag77910 Human lac
6	70	100.0	689	AAW71181	Aaw71181 Mutant hu
7	70	100.0	688	AAW77909	Aag77909 Human lac
8	70	100.0	690	AAW71180	Aaw71180 Mutant hu
9	70	100.0	690	AAW77908	Aag77908 Human lac
10	70	100.0	690	ABG80724	ABG80724 Codon opt
11	70	100.0	690	AAE27884	Aae27884 Human cod
12	70	100.0	692	AAW58733	Aaw58733 Human lac
13	70	100.0	692	AAW97382	Aaw97382 Human lac
14	70	100.0	692	AAW77906	Aag77906 Human lac
15	70	100.0	692	AAE28002	Aae28002 Human cod
16	70	100.0	693	AAW85146	Aaw85146 Lactoferr
17	70	100.0	705	AAW85146	Aaw85146 Human lac
18	70	100.0	705	AAW31152	Aaw31152 Human lac
19	70	100.0	708	AAW22423	Aaw22423 Human lac
20	70	100.0	708	AAW31153	Aaw31153 Human lac
21	70	100.0	709	AAW1583	Aaw1583 Lactoferr
22	70	100.0	709	AAW45198	Aaw45198 Human lac
23	70	100.0	709	AAW45199	Aaw45199 Human lac
24	70	100.0	709	AAW21695	Aaw21695 Human lac
25	70	100.0	709	AAW53879	Aaw53879 Human lac

26	70	100.0	709	AAW77577	Aaw77577 Human lac
27	70	100.0	709	AAW03830	Aaw03830 Human lac
28	70	100.0	709	AAW36842	Aaw36842 Protein e
29	70	100.0	709	AAW76659	Aaw76659 Human lac
30	70	100.0	711	AAW08033	Aaw08033 Human lac
31	70	100.0	711	AAW43653	Aaw43653 Lactoferr
32	70	100.0	711	AAW09342	Aaw09342 Human lac
33	70	100.0	711	AAW57317	Aaw57317 Human lac
34	70	100.0	711	AAW53880	Aaw53880 Bovine al
35	70	100.0	711	AAW6021	Aaw6021 Human lac
36	70	100.0	711	AAW77578	Aaw77578 Human lac
37	70	100.0	711	AAW03831	Aaw03831 Human lac
38	70	100.0	711	AAW08182	Aaw08182 Amino ac1
39	70	100.0	711	AAW36843	Aaw36843 Human lac
40	70	100.0	711	AAW02341	Aaw02341 Human lac
41	70	100.0	711	AAW64828	Aaw64828 Chronic h
42	70	100.0	711	AAW76661	Aaw76661 Human lac
43	65	92.9	12	AAW93878	Aaw93878 Bifidobac
44	58	82.9	685	AAW11664	Aaw11664 Partial p
45	58	82.9	685	AAW11663	Aaw11663 Partial p

ALIGNMENTS

RESULT 1
AAW93880
ID AAW93880 standard; peptide; 13 AA.

AC AAW93880;
DT 27-AUG-2003 (revised)
DI 25-JUN-1999 (first entry)
DE Bifidobacterium bifidus stimulating peptide 16.

KM Bifidogenic peptide; protease; treatment; microbe-related disease;
KW bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
KW infection; inflammation; microbial induced tumour; degenerative disorder;
KW diarrhoea; colic; oral microflora; intestinal microflora; caries;
KW vaginal microflora.

OS Bifidobacterium bifidum.

PN WO9914231-A2.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-EP005899.

PR 16-SEP-1997; 97DE-01040604.

PR 11-FEB-1998; 98DE-01005385.

PA (FORS/) FORSMANN W.

PI Forssmann W, Zucht H, Liepke C;

DR WPI, 1999-244022/20.

PT Milk-derived peptides that stimulate Bifidobacterium bifidus.

PS Claim 2; Page 3; 25pp; German.

XX This invention describes milk-derived bifidogenic peptides and their
XX active derivatives or fragments, and combinations of them produced by
XX chemical coupling. Such are produced from bovine or human milk by
XX treatment for 2 hr with proteases, then centrifuging to remove fat and
XX acidifying to pH 2 to precipitate proteins. The supernatant phase is then
XX subjected to reverse-phase high-performance liquid chromatography (HPLC)
XX and carbon-exchange HPLC, the fractions adjusted to salt content below 25
XX mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
XX Bifidobacterium bifidus and Escherichia coli in presence of the
XX fractions. Those fractions for which (Bw-B0)-(Ew-E0) is at least 0.15 are

CC selected where Bw = germ count after 16 hr culture of *B. bifidus* in 50%
 CC Elliker broth containing peptide at 0.2 mg/ml, B0 = germ count under
 CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of *B. coli* in 3 g/l tryptic broth containing peptide at 0.2
 CC mg/ml. B0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W93888 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or carrier. (Updated on 27-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 70; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARRARVWCAVGE 13
 DB 1 ARRARVWCAVGE 13
 RESULT 2
 ID AAW71183 standard; protein; 687 AA.
 XX
 AC AAW71183;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Mutant human lactoferrin protein designated hLF-5N.
 XX
 KW Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
 KW anti-infective; coagulant; complement activation; inhibition;
 KW LPS mediated activation; myelopoiesis; growth promotion;
 KW intestinal epithelial cell; hydroxyl-radical formation;
 KW intestinal iron uptake; excretion.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 PN MO9833509-A2.
 PD 06-AUG-1998.
 PF 02-FEB-1998; 98WO-IB000441.
 PR 03-FEB-1997; 97US-0036859P.
 PR 02-FEB-1998; 98US-00017043.
 XX
 PA (PHAR-) PHARMING BV.
 PI Nuijens J, Van Berkel PHC;
 DR WPI; 1998-437164/37.
 XX
 PT Compositions containing human lactoferrin and variants - are used for
 PT treating e.g. anaemia, iron-storage disease, inflammation, tumours,
 PT rheumatoid arthritis, ulcerative colitis or infections.
 XX
 PS Claim 2; Page; 70pp; English.
 XX
 CC AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
 CC The lactoferrin variants bind heparin with lower affinity than natural
 CC lactoferrin. The lactoferrin variants exhibit biological activities such
 CC as anti-inflammatory, anti-viral and anti-infective activities as well as
 CC a pro- and anti-coagulant effects, modulation of complement activation,
 CC inhibition of LPS mediated activation of neutrophils, inhibition of
 CC myelopoiesis, regulation of transcription, growth promotion of intestinal
 CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
 CC intestinal iron uptake and excretion. Note: this sequence does not appear
 CC in the specification; it was created using information provided

XX Sequence 687 AA;
 SQ
 Query Match 100.0%; Score 70; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARRARVWCAVGE 13
 DB 336 ARRARVWCAVGE 348
 RESULT 3
 ID AAG77911 standard; protein; 687 AA.
 XX
 AC AAG77911;
 XX
 DT 22-JAN-2002 (first entry)
 XX
 DE Human lactoferrin variant hLF-5N.
 XX
 KW Human; lactoferrin; hLF; infectious disease; inflammatory disease;
 KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
 KW anaemia; myelopoiesis; reperfusion injury; cytokine release; proteoglycan;
 KW hLF-5N; mutant; mucin.
 XX
 OS Homo sapiens.
 OS
 FT Key Location/Qualifiers
 FT 23..26
 FT Domain /label=Cationic_domain
 XX
 PN MO200172322-A2.
 PD 04-OCT-2001.
 PF 27-MAR-2001; 2001WO-NL000253.
 PR 27-MAR-2000; 2000EP-00201110.
 PR 27-MAR-2000; 2000US-0193352P.
 XX
 PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
 PI Van Bree JBM, Nuijens JH;
 DR WPI; 2001-648424/74.
 XX
 PT Use of lactoferrin for treatment of infectious diseases, inflammatory
 PT diseases and excess of heparin.
 XX
 PS Claim 10; Page; 49pp; English.
 XX
 CC The sequence represents the human lactoferrin (hLF) protein variant hLF-
 CC 5N. The invention relates to novel methods of treatment using high doses
 CC of lactoferrin. The methods of the invention are useful for the treatment
 CC or prophylaxis of infectious diseases, inflammatory diseases and excess
 CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
 CC anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and
 CC proteoglycan-mediated entry of virus into cells. The advantage of the
 CC method is that the patient is substantially free of side effect responses
 CC to administration of lactoferrin. Therefore large doses of lactoferrin
 CC can be administered. Note: The present sequence is not shown in the
 CC specification but is derived from human wild-type lactoferrin sequence
 CC given in the sequence listing of the specification
 XX
 SQ Sequence 687 AA;
 Query Match 100.0%; Score 70; DB 4; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARRARVWCAVGE 13


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Db          336 ARRAVWCAVGE 348
|||||
RESULT 4
AAW71182
ID AAW71182 standard; protein; 688 AA.
XX
XX AAW71182;
AC
XX 27-OCT-1998 (first entry)
XX
XX Mutant human lactoferrin protein designated hLF-4N.
DE
XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
XX anti-infective; coagulant; complement activation; inhibition;
XX LPS mediated activation; myeloperoxidase; growth promotion;
XX intestinal epithelial cell; hydroxyl-radical formation;
XX intestinal iron uptake; excretion.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX MO9835509-A2.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998; 98MO-IB000441.
XX
XX 03-FEB-1997; 97US-0036859P.
XX
XX 02-FEB-1998; 98US-00017043.
XX
XX (PHAR-) PHARMING BV.
XX
XX Nuijens J, Van Berkel PHC;
XX
XX WPI; 1998-437164/37.
XX
XX Compositions containing human lactoferrin and variants - are used for
XX treating e.g. anaemia, iron-storage disease, inflammation, tumours,
XX rheumatoid arthritis, ulcerative colitis or infections.
XX
XX PS Claim 2; Page; 70pp; English.
XX
XX AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
XX The lactoferrin variants bind heparin with lower affinity than natural
XX lactoferrin. The lactoferrin variants exhibit biological activities such
XX as anti-inflammatory, anti-viral and anti-infective activities as well as
XX a pro- and anti-coagulant effects, modulation of complement activation,
XX inhibition of LPS mediated activation of neutrophils, inhibition of
XX myeloperoxidase, regulation of transcription, growth promotion of intestinal
XX epithelial cells, inhibition of hydroxyl-radical formation, and a role in
XX intestinal iron uptake and excretion. Note: this sequence does not appear
XX in the specification; it was created using information provided
XX
XX Sequence 688 AA;
SQ
Query Match          100.0%; Score 70; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX
XX Human lactoferrin variant hLF-4N.
DE
XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
XX excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
XX anaemia; myeloperoxidase; reperfusion injury; cytokine release; proteoglycan;
XX hLF-4N; mutant; mucin.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 24..27
XX FT /label= Cationic_domain
XX
XX MO200172322-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001MO-NL000253.
XX
XX 27-MAR-2000; 2000EP-00201110.
XX
XX 27-MAR-2000; 2000US-0193352P.
XX
XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX
XX Van Bree JBM, Nuijens JH;
XX
XX WPI; 2001-648424/74.
XX
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
XX diseases and excess of heparin.
XX
XX PS Claim 10; Page; 49pp; English.
XX
XX The sequence represents the human lactoferrin (hLF) protein variant hLF-
XX 4N. The invention relates to novel methods of treatment using high doses
XX of lactoferrin. The methods of the invention are useful for the treatment
XX or prophylaxis of infectious diseases, inflammatory diseases and excess
XX of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
XX anaemia, myeloperoxidase, reducing reperfusion injury, cytokine release and
XX proteoglycan-mediated entry of virus into cells. The advantage of the
XX method is that the patient is substantially free of side effect responses
XX to administration of lactoferrin. Therefore large doses of lactoferrin
XX can be administered. Note: The present sequence is not shown in the
XX specification but is derived from human wild-type lactoferrin sequence
XX given in the sequence listing of the specification
XX
XX SQ Sequence 688 AA;
SQ
Query Match          100.0%; Score 70; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ARRAVWCAVGE 13
DB 337 ARRAVWCAVGE 349
RESULT 5
AAG77910
ID AAG77910 standard; protein; 688 AA.
XX
XX AAG77910;
XX
XX 22-JAN-2002 (first entry)

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OY 1 ARRAVWCAVGE 13
DB 337 ARRAVWCAVGE 349
RESULT 6
AAW71181
ID AAW71181 standard; protein; 689 AA.
XX
XX AAW71181;
XX
XX 27-OCT-1998 (first entry)
XX
XX Mutant human lactoferrin protein designated hLF-3N.
XX
XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
XX anti-infective; coagulant; complement activation; inhibition;
XX LPS mediated activation; myeloperoxidase; growth promotion;
XX intestinal epithelial cell; hydroxyl-radical formation;
XX intestinal iron uptake; excretion.

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XX OS Synthetic.
XX OS Homo sapiens.
XX XX MO9833509-A2.
XX XX 06-AUG-1998.
XX XX 02-FEB-1998; 98WO-IB000441.
XX XX 03-FEB-1997; 97US-0036859P.
XX XX 02-FEB-1998; 98US-00017043.
XX PA (PHAR-) PHARMING BV.
XX FI Nuijens J, Van Berkel PHC;
XX DR WPI; 1998-437164/37.
XX PT Compositions containing human lactoferrin and variants - are used for
PT treating e.g. anaemia, iron storage disease, inflammation, tumours,
PT rheumatoid arthritis, ulcerative colitis or infections.
XX PS Claim 2; Page; 70pp; English.
XX CC AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
CC CC The lactoferrin variants bind heparin with lower affinity than natural
CC CC lactoferrin. The lactoferrin variants exhibit biological activities such
CC CC as anti-inflammatory, anti-viral and anti-infective activities as well as
CC CC a pro- and anti-coagulant effects, modulation of complement activation,
CC CC inhibition of LPS mediated activation of neutrophils, inhibition of
CC CC myelopoiesis, regulation of transcription, growth promotion of intestinal
CC CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
CC CC intestinal iron uptake and excretion. Note: this sequence does not appear
CC CC in the specification; it was created using information provided
SQ Sequence 689 AA;

Query Match 100.0%; Score 70; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ARRARVVMCAVGE 13
DB 338 ARRARVVMCAVGE 350

RESULT 7
AAG77909
ID AAG77909 standard; protein; 689 AA.
XX AC AAG77909;
XX DT 22-JAN-2002 (first entry)
XX DE Human lactoferrin variant hLF-3N.
XX XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
XX KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
XX KW anaemia; myelopoiesis; reperfusion injury; cytokine release; proteoglycan;
XX KW mutant; mutant; hLF-3N; mutant; mutant.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 25..28
XX XX /label= Cationic_domain
XX PN WO200172322-A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-NL000253.

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XX XX 27-MAR-2000; 2000EP-00201110.
XX PR 27-MAR-2000; 2000US-0193352P.
XX XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
XX XX Van Bree JBMV, Nuijens JH;
XX XX WPI; 2001-648424/74.
XX DR Use of lactoferrin for treatment of infectious diseases, inflammatory
XX PT diseases and excess of heparin.
XX PS Claim 10; Page; 49pp; English.
XX CC The sequence represents the human lactoferrin (hLF) protein variant hLF-
XX CC 3N. The invention relates to novel methods of treatment using high doses
XX CC of lactoferrin. The methods of the invention are useful for the treatment
XX CC of prophylaxis of infectious diseases, inflammatory diseases and excess
XX CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
XX CC anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and
XX CC proteoglycan-mediated entry of virus into cells. The advantage of the
XX CC method is that the patient is substantially free of side effect responses
XX CC to administration of lactoferrin. Therefore large doses of lactoferrin
XX CC can be administered. Note: The present sequence is not shown in the
XX CC specification but is derived from human wild-type lactoferrin sequence
XX CC given in the sequence listing of the specification
SQ Sequence 689 AA;

Query Match 100.0%; Score 70; DB 4; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ARRARVVMCAVGE 13
DB 338 ARRARVVMCAVGE 350

RESULT 8
AAW71180
ID AAW71180 standard; protein; 690 AA.
XX AC AAW71180;
XX DT 27-OCT-1998 (first entry)
XX DE Mutant human lactoferrin protein designated hLF-2N.
XX XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
XX KW anti-infective; coagulant; complement activation; inhibition;
XX KW LPS mediated activation; myelopoiesis; growth promotion;
XX KW intestinal epithelial cell; hydroxyl-radical formation;
XX KW intestinal iron uptake; excretion.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9833509-A2.
XX XX 06-AUG-1998.
XX XX 02-FEB-1998; 98WO-IB000441.
XX XX 03-FEB-1997; 97US-0036859P.
XX XX 02-FEB-1998; 98US-00017043.
XX PA (PHAR-) PHARMING BV.
XX XX Nuijens J, Van Berkel PHC;
XX PI WPI; 1998-437164/37.

```

PT Compositions containing human lactoferrin and variants - are used for
PT treating e.g. anemia, iron-storage disease, inflammation, tumours,
PT rheumatoid arthritis, ulcerative colitis or infections.
XX
XX Claim 2; Page; 70pp; English.
PS
CC AA071180-83 represent N-terminally truncated human lactoferrin proteins.
CC The lactoferrin variants bind heparin with lower affinity than natural
CC lactoferrin. The lactoferrin variants exhibit biological activities such
CC as anti-inflammatory, anti-viral and anti-infective activities as well as
CC inhibition of LPS mediated activation of neutrophils, inhibition of
CC myeloperoxidase, regulation of transcription, growth promotion of intestinal
CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
CC intestinal iron uptake and excretion. Note: this sequence does not appear
CC in the specification; it was created using information provided
XX
XX
SQ Sequence 690 AA;

Query Match 100.0%; Score 70; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARVWCAVGE 13
| | | | | | | | | | | | | | |
Db 339 ARRARVWCAVGE 351

RESULT 9
AAG77908
ID AAG77908 standard; protein; 690 AA.
XX
XX AAG77908;
AC
XX
XX 22-JAN-2002 (first entry)
DT
XX
XX Human lactoferrin variant hLF-2N.
DE
XX
XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
KW anaemia; myeloperoxidase; reperfusion injury; cytokine release;
XX proteoglycan; hLF-2N; mutant; mutein.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Domain 26..29
FT /label=Cationic_domain
XX
XX WO200172322-A2.
XX
XX
XX 04-OCT-2001.
PD
XX 27-MAR-2001; 2001MO-NU000253.
PF
XX 27-MAR-2000; 2000EP-00201110.
PR 27-MAR-2000; 2000US-0193352P.
XX
XX (PHAR-) PHARWING INTELLECTUAL PROPERTY BV.
PA
XX
XX Van Bree JBM, Nuijens JH;
PI
XX WPI; 2001-648424/74.
DR
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
PT diseases and excess of heparin.
XX
XX Claim 10; Page; 49pp; English.
PS
CC The sequence represents the human lactoferrin (hLF) protein variant hLF-
CC 2N. The invention relates to novel methods of treatment using high doses
CC of lactoferrin. The methods of the invention are useful for the treatment
CC or prophylaxis of infectious diseases, inflammatory diseases and excess

CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
CC anaemia, myeloperoxidase, reducing reperfusion injury, cytokine release and
CC proteoglycan-mediated entry of virus into cells. The advantage of the
CC method is that the patient is substantially free of side effect responses
CC to administration of lactoferrin. Therefore large doses of lactoferrin
CC can be administered. Note: The present sequence is not shown in the
CC specification but is derived from human wild-type lactoferrin sequence
XX given in the sequence listing of the specification
XX
XX
SQ Sequence 690 AA;

Query Match 100.0%; Score 70; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARVWCAVGE 13
| | | | | | | | | | | | | | |
Db 339 ARRARVWCAVGE 351

RESULT 10
ABG80724
ID ABG80724 standard; protein; 690 AA.
XX
XX ABG80724;
AC
XX
XX 29-NOV-2002 (first entry)
DT
XX
XX Codon optimised lactoferrin protein.
DE
XX
XX Transformed plant; heterologous transcription factor; transgenic plant;
KW seed protein; protein expression.
XX
XX Homo sapiens.
OS
XX
XX WO200264750-A2.
PN
XX
XX 22-AUG-2002.
PD
XX
XX 14-FEB-2002; 2002MO-US004909.
PF
XX
XX 14-FEB-2001; 2001US-0269188P.
PR 14-FEB-2001; 2001US-0269198P.
PR 02-MAY-2001; 2001US-00847232.
XX
XX (VENT-) VENTRIA BIOSCIENCE.
PA
XX
XX Huang N, Yang D;
PI
XX
XX WPI; 2002-657592/70.
DR N-PSDB; ABS66515.
DR
XX
XX Producing heterologous polypeptide in plant grain, by culturing
PT transformed plant to form a grain-producing transforming plant, and
PT recovering transgenic grains containing polypeptide from transformed
PT plant.
XX
XX
XX Exemple 15; Page 117; 230pp; English.
PS
XX
XX The invention describes a method of producing a heterologous polypeptide
CC (I) in a grain of a plant, comprising culturing a transformed plant (PI)
CC comprising a first chimeric gene, and optionally, at least one
CC heterologous transcription factor that is capable of enhancing the
CC expression of the chimeric gene, to form a grain producing transforming
CC plant (P2), and recovering transgenic grains containing (I) from P2. The
CC method is useful for producing heterologous polypeptide in a grain of a
CC plant. (I) is a non-plant storage, human or non-human animal, milk or
CC other than a milk polypeptide, antibodies, cytokines, lymphokines,
CC chemokines, hormones, growth factors, coagulation factors, anti-
CC infectives, or cytotoxins, or anti-inflammatory molecule or intestinal
CC trefoil factor (ITF) or its active fragment. Preferably, (I) is
CC lactoferrin, lyszyme, lactoferricin, ITF, epidermal growth factor (EGF),
CC keratinocyte growth factor (KGF), insulin-like growth factor I (IGF-I),

CC lactoferrin, kappa-casein, haptocorrin, lactoperoxidase, alpha-1-
 CC antitrypsin, immunoglobulins, alpha-lactalbumin, beta-lactoglobulin,
 CC alpha-casein, beta-casein, albumin, fibrinogen or protease inhibitor.
 CC This is the amino acid sequence of a protein associated with method of
 CC producing a transgenic plant
 XX
 SQ Sequence 690 AA;

Query Match 100.0%; Score 70; DB 5; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVWCAVGE 13
 DB 339 ARRAVWCAVGE 351

RESULT 11
 ID AAE27884 standard; protein; 690 AA.

AC AAE27884;
 DT 27-DEC-2002 (first entry)
 DE Human codon optimised lactoferrin.
 XX
 XX Human, feed improvement; plant-derived feed; antibiotic; additive;
 XX anti-microbial; poultry; lactoferrin; flour; malt.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Msc-difference 319.320
 FT /note="Encoded by CTG TAC CTC"

W0200263975-A2.

22-AUG-2002.

14-FEB-2002; 2002MO-US004919.

14-FEB-2001; 2001US-0269188P.

02-MAY-2001; 2001US-00847232.

(VENT-) VENTRIA BIOSCIENCE.

Huang N, Rodriguez RU, Hagie FE;

WPI; 2002-682708/73.

N-PSDB; AAD45297.

XX Improved feed for production animals, comprising plant-derived feed
 PT ingredients, and seed composition containing flour, extract, or malt from
 PT mature monocot seeds and heterologous seed-produced anti-microbial
 PT proteins.

Example 7; Page 148-150; 175pp; English.

CC The invention relates to improved feed for production animals, comprising
 CC one or more plant-derived feed ingredients, substantially unsupplemented
 CC with small-molecule antibiotics and as an additive a seed composition
 CC containing a flour, extract or malt obtained from mature monocot seeds
 CC and one or more heterologous seed-produced anti-microbial proteins in
 CC substantially unpurified form. The invention is useful as a feed for
 CC production animals such as poultry and hoofed farm animals. The present
 CC sequence is human codon optimised lactoferrin. This sequence is used in
 CC the invention

Sequence 690 AA;

Query Match 100.0%; Score 70; DB 5; Length 690;

Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVWCAVGE 13
 DB 339 ARRAVWCAVGE 351

RESULT 12
 ID AAY58733 standard; protein; 692 AA.

AC AAY58733;
 DT 25-APR-2000 (first entry)

DE Human lactoferrin.
 XX
 XX Lactoferrin; human; transgenic plant.

OS Homo sapiens.

W0200004146-A1.

27-JAN-2000.

19-JUL-1999; 99WO-IT000226.

17-JUL-1998; 98IT-RM000478.

(PLAN-) PLANTECHNO SRL.

Fogher C;

WPI; 2000-161129/14.

N-PSDB; AAZ58122.

XX Synthetic polynucleotide encoding human lactoferrin, used for production
 PT of functional foods, vegetal milks and human lactoferrin.

Dislosure; Page 73-77; 93pp; English.

CC The present sequence is that of human lactoferrin. The invention relates
 CC to a synthetic gene (see AAZ58122) that encodes human lactoferrin but
 CC which has codon usage designed to maximize expression in plants.
 CC Transgenic plants that express human lactoferrin in a tissue-specific
 CC manner, especially in the seeds, can be used in processes for the
 CC production of functional vegetal milk, fruit juices, fruit and/or
 CC vegetable homogenized foods (claimed). The transgenic plants are selected
 CC from solanaceae, cereals, leguminosae, fruit bearing plants and
 CC horticultural plants, especially soybean, tobacco and rice

Sequence 692 AA;

Query Match 100.0%; Score 70; DB 3; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVWCAVGE 13
 DB 341 ARRAVWCAVGE 353

RESULT 13
 ID AAB97382 standard; protein; 692 AA.

AAB97382;

17-AUG-2001 (first entry)

Human lactoferrin (hLF).


```

XX 22-AUG-2002.
PD
XX
PF 14-FEB-2002; 2002MO-US004921.
XX
PR 14-FEB-2001; 2001US-0269199P.
PR 02-MAY-2001; 2001US-00847232.
XX
PA (VENT-) VENTRIA BIOSCIENCE.
XX
PI Huang N, Rodriguez RL, Hagie FE;
XX
DR WPI; 2002-667011/71.
DR N-PSDB; AAD44922.
XX
PI New nutritionally enhanced food compositions, useful for improving infant
PT formula, or supplementing or enhancing the diet of infants, particularly
PT very-low birth weight infants.
XX
PS Example 9; Page 104; 179pp; English.
XX
CC The invention relates to a nutritionally enhanced food comprising one or
CC more plant-derived food ingredients, and as an additive, a seed
CC composition containing a flour, extract, or malt obtained from mature
CC monocot seeds and one or more seed-produced human milk proteins in
CC substantially unpurified form. The nutritionally enhanced food and food
CC additive compositions are useful for improving infant formula, infant
CC formulas containing the recombinant human milk proteins are useful in
CC supplementing or enhancing the diet of infants, particularly very-low
CC birth weight infants. The present sequence is human codon optimised
CC lactoferrin
XX
SQ Sequence 692 AA;

Query Match          100.0%; Score 70; DB 5; Length 692;
Best Local Similarity 100.0%; Pred.No. 0.00073;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARRARVVMCAVGE 13
      |||||
Db      341 ARRARVVMCAVGE 353

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Search completed: September 1, 2004, 00:09:44
 Job time : 32.2867 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:04:10 : Search time 8.40667 Seconds
(without alignments)
79.834 Million cell updates/sec

Title: US-09-508-095-16
Perfect score: 70
Sequence: 1 ARRAVWCAVGE 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCOTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	70	100.0	694	3 US-08-724-586-2	Sequence 2, Appl1
2	70	100.0	694	3 US-09-421-632-2	Sequence 2, Appl1
3	70	100.0	694	4 US-09-992-190-2	Sequence 2, Appl1
4	70	100.0	705	2 US-08-655-640-2	Sequence 2, Appl1
5	70	100.0	708	2 US-08-655-640-4	Sequence 4, Appl1
6	70	100.0	709	1 US-08-154-019-2	Sequence 2, Appl1
7	70	100.0	709	1 US-08-461-333-2	Sequence 2, Appl1
8	70	100.0	709	3 US-08-461-333-2	Sequence 2, Appl1
9	70	100.0	709	3 US-09-158-313-2	Sequence 2, Appl1
10	70	100.0	709	3 US-08-476-798-2	Sequence 2, Appl1
11	70	100.0	711	1 US-08-145-681-2	Sequence 2, Appl1
12	70	100.0	711	1 US-08-250-308-2	Sequence 2, Appl1
13	70	100.0	711	1 US-08-154-019-4	Sequence 4, Appl1
14	70	100.0	711	1 US-08-461-333-4	Sequence 4, Appl1
15	70	100.0	711	1 US-08-453-703-2	Sequence 2, Appl1
16	70	100.0	711	2 US-08-453-703-2	Sequence 2, Appl1
17	70	100.0	711	2 US-08-464-167-4	Sequence 4, Appl1
18	70	100.0	711	3 US-08-456-108-4	Sequence 4, Appl1
19	70	100.0	711	3 US-09-158-313-4	Sequence 4, Appl1
20	70	100.0	711	3 US-08-456-108-2	Sequence 4, Appl1
21	70	100.0	711	3 US-08-476-798-4	Sequence 4, Appl1
22	70	100.0	711	4 US-09-265-577-2	Sequence 2, Appl1
23	70	100.0	711	4 US-09-633-739-2	Sequence 2, Appl1
24	70	100.0	711	5 PCT-US93-03614-2	Sequence 6, Appl1
25	58	82.9	703	1 US-08-145-681-6	Sequence 6, Appl1
26	58	82.9	703	1 US-08-453-703-6	Sequence 6, Appl1
27	58	82.9	703	1 US-08-456-106-6	Sequence 6, Appl1
	58	82.9	703	3 US-08-456-108-6	Sequence 6, Appl1

28	58	82.9	703	3 US-09-265-577-6	Sequence 6, Appl1
29	58	82.9	703	4 US-09-633-739-6	Sequence 6, Appl1
30	54	77.1	708	1 US-08-145-681-4	Sequence 4, Appl1
31	54	77.1	708	1 US-08-453-703-4	Sequence 4, Appl1
32	54	77.1	708	2 US-08-456-106-4	Sequence 4, Appl1
33	54	77.1	708	2 US-08-456-108-4	Sequence 4, Appl1
34	54	77.1	708	3 US-09-265-577-4	Sequence 4, Appl1
35	54	77.1	708	3 US-09-633-739-4	Sequence 4, Appl1
36	44	62.9	135	4 US-09-252-991A-23456	Sequence 23456, A
37	43	61.4	290	4 US-09-328-352-5309	Sequence 5309, A
38	43	61.4	406	4 US-09-252-991A-21445	Sequence 21445, A
39	42	60.0	264	4 US-09-252-991A-26707	Sequence 26707, A
40	41	58.6	884	4 US-08-464-182A-21	Sequence 21, Appl1
41	40	57.1	25	2 US-08-464-182A-4	Sequence 21, Appl1
42	40	57.1	25	2 US-08-464-182A-4	Sequence 21, Appl1
43	40	57.1	30	2 US-08-464-182A-4	Sequence 4, Appl1
44	40	57.1	30	2 US-08-464-182A-4	Sequence 4, Appl1
45	40	57.1	47	2 US-08-464-182A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-724-586-2
; Sequence 2, Application US/08724586
; Patent No. 6066469
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kruzel, Tomasz
; APPLICANT: Golinick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-724-586-2

Query Match 100.0%; Score 70; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 ARRAVWCAVGE 13

Db 343 ARARVTWCAGE 355

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1  RESULT 2
2  US-09-421-632-2
3  / Sequence 2, Application US/09421632
4  / Patent No. 6277817
5  / GENERAL INFORMATION:
6  / APPLICANT: Krugel, Marian L.
7  / APPLICANT: Kurecki, Tomasz
8  / APPLICANT: Gollnick, Paul D.
9  / APPLICANT: Doyle, Darrell J.
10 / TITLE OF INVENTION: Cloning, Expression, and Uses of Human
11 / TITLE OF INVENTION: Lactoferrin
12 / NUMBER OF SEQUENCES: 8
13 / CORRESPONDENCE ADDRESSES:
14 / ADDRESSEE: Jacobson, Price, Holman & Stern
15 / STREET: 400 Seventh St. N.W.
16 / CITY: Washington D.C.
17 / COUNTRY: U.S.A.
18 / ZIP: 20004
19 / COMPUTER READABLE FORM:
20 / MEDIUM TYPE: floppy disk
21 / COMPUTER: IBM PC compatible
22 / OPERATING SYSTEM: PC-DOS/MS-DOS
23 / SOFTWARE: PatentIn Release #1.0, Version #1.25
24 / CURRENT APPLICATION DATA:
25 / APPLICATION NUMBER: US/09/421,632
26 / FILING DATE:
27 / CLASSIFICATION:
28 / PRIOR APPLICATION DATA:
29 / APPLICATION NUMBER: 08/724,586
30 / FILING DATE:
31 / ATTORNEY/AGENT INFORMATION:
32 / NAME: Player, William E.
33 / REGISTRATION NUMBER: 31,409
34 / REFERENCE/DOCKET NUMBER: 10505/P58185C
35 / TELECOMMUNICATION INFORMATION:
36 / TELEPHONE: (202) 638-6666
37 / TELEFAX: (202) 393-5350
38 / INFORMATION FOR SEQ ID NO: 2:
39 / SEQUENCE CHARACTERISTICS:
40 / LENGTH: 694 amino acids
41 / TYPE: amino acid
42 / TOPOLOGY: linear
43 / MOLECULE TYPE: protein
44 / US-09-421-632-2

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RESULT 3
US-09-932-190-2
Sequence 2, Application US/09932190
Patent No. 645687
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
Kurecki, Tomasz
Gollnick, Paul D.
Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.

CITY: Washington D.C.
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/932,190
 FILING DATE: 17-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/724,586
 FILING DATE: 30-SEPT-1996
 APPLICATION NUMBER: US 08/238,445
 FILING DATE: 05-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Player, William E.
 REGISTRATION NUMBER: 31,409
 REFERENCE/DOCKET NUMBER: 10505/P58185C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-6666
 TELEFAX: (202) 393-5350
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 694 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 GS-09-932-190-2

RESULT 4
US-08-655-640-2
Sequence 2, Application US/08655640
Patent No. 5948613
GENERAL INFORMATION:
APPLICANT: Teng, Christina
APPLICANT: Pamela, Timothy J.
TITLE OF INVENTION: HUMAN LACOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DAREY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-640-2

Query Match 100.0%; Score 70; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRAVWCAYGE 13
Db 358 ARRAVWCAYGE 370

RESULT 5
US-08-655-640-4
Sequence 4, Application US/08655640
Patent No. 5948613
GENERAL INFORMATION:
APPLICANT: Teng, Christina
APPLICANT: Panela, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-640-4

Query Match 100.0%; Score 70; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRAVWCAYGE 13
Db 358 ARRAVWCAYGE 372

RESULT 6
US-08-154-019-2
Sequence 2, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheut, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-154-019-2

Query Match 100.0%; Score 70; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRAVWCAYGE 13
Db 358 ARRAVWCAYGE 370

RESULT 7
US-08-461-333-2

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Sequence 2, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-333-2

Query Match 100.0%; Score 70; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 358 ARARVWCAGE 370

RESULT 8
US-08-464-167-2
Sequence 2, Application US/0846167
Patent No. 6013857
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
```

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APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-167-2

Query Match 100.0%; Score 70; DB 3; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
Db 358 ARARVWCAGE 370

RESULT 9
US-09-158-313-2
Sequence 2, Application US/09158313
Patent No. 6066725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
```

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-313-2
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Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
Db 358 ARARVWCAGE 370

RESULT 10
US-08-476-798-2
Sequence 2, Application US/08476798
Patent No. 6140552
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-798-2
Query Match 100.0%; Score 70; DB 3; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
Db 358 ARARVWCAGE 370

RESULT 11
US-08-145-681-2
Sequence 2, Application US/08145681
Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/145,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGregor, Martin L.
REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/229/1522
TELEFAX: 713/229/1874
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: H. sapiens
US-08-145-681-2

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ARARVWCAGE 13
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DB 360 ARARVWCAGE 372

RESULT 12
US-08-250-308-2
Sequence 2, Application US/08250308
Patent No. 5571896
Patent No. 5571896 5571896
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Production of Recombinant Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney St.
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,308
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,304
FILING DATE: 24-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/6515587
TELEFAX: 713/6515246
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-250-308-2

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 360 ARARVWCAGE 372

RESULT 13
US-08-154-019-4
Sequence 4, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platendburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liedeschultz, Jce O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-154-019-4

Wed Sep 1 08:24:07 2004

us-09-508-095-16.aug31.ra1

Page 7

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARARVWCAGE 13
Db 360 ARARVWCAGE 372

RESULT 14
US-08-461-333-4
Sequence 4, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krumpfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-333-4

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARARVWCAGE 13
Db 360 ARARVWCAGE 372

Db 360 ARARVWCAGE 372

RESULT 15
US-08-453-703-2
Sequence 2, Application US/08453703
Patent No. 5766939
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
Virus Vectors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: H. sapiens
US-08-453-703-2

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 360 ARARVWCAGE 372

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Job time : 8.40667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:15:50 ; Search time 29.64 Seconds
(without alignments)
137.988 Million cell updates/sec

Title: US-09-508-095-16
Perfect score: 70
Sequence: 1 ARRAVWCAVGE 13

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:*

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- 2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	70	100.0	690	14 US-10-076-816-4	Sequence 4, Appl
3	70	100.0	690	14 US-10-077-381-4	Sequence 4, Appl
4	70	100.0	690	14 US-10-639-835-4	Sequence 4, Appl
5	70	100.0	694	13 US-10-023-096-2	Sequence 2, Appl
6	70	100.0	709	14 US-10-170-221-2	Sequence 2, Appl
7	70	100.0	711	14 US-10-169-297-9	Sequence 2, Appl
8	70	100.0	711	14 US-10-170-221-4	Sequence 2, Appl
9	70	100.0	711	15 US-10-341-434-202	Sequence 202, Appl
10	70	100.0	711	15 US-10-341-434-218	Sequence 218, Appl
11	70	100.0	711	15 US-10-440-464-69	Sequence 69, Appl
12	70	100.0	711	16 US-10-408-7654-2000	Sequence 2000, Appl
13	54	77.1	234	14 US-10-169-297-35	Sequence 35, Appl
14	54	77.1	708	14 US-10-169-297-8	Sequence 8, Appl
15	46	65.7	77	9 US-09-738-626-3901	Sequence 3901, Appl

16	44	62.9	60	16	US-10-437-963-147215	Sequence 147215
17	44	62.9	705	16 <td>US-09-847-208-102<td>Sequence 102, Appl</td></td>	US-09-847-208-102 <td>Sequence 102, Appl</td>	Sequence 102, Appl
18	41	58.6	77	16 <td>US-10-437-963-158618<td>Sequence 158618, A</td></td>	US-10-437-963-158618 <td>Sequence 158618, A</td>	Sequence 158618, A
19	41	58.6	254	14 <td>US-10-156-761-10952<td>Sequence 10952, A</td></td>	US-10-156-761-10952 <td>Sequence 10952, A</td>	Sequence 10952, A
20	41	58.6	355	14 <td>US-10-424-599-265471<td>Sequence 265471, A</td></td>	US-10-424-599-265471 <td>Sequence 265471, A</td>	Sequence 265471, A
21	41	58.6	424	12 <td>US-10-425-114-49461<td>Sequence 49461, A</td></td>	US-10-425-114-49461 <td>Sequence 49461, A</td>	Sequence 49461, A
22	41	58.6	424	16 <td>US-10-437-963-133123<td>Sequence 133123, A</td></td>	US-10-437-963-133123 <td>Sequence 133123, A</td>	Sequence 133123, A
23	40.5	57.9	460	12 <td>US-10-425-114-50342<td>Sequence 50342, A</td></td>	US-10-425-114-50342 <td>Sequence 50342, A</td>	Sequence 50342, A
24	40	57.1	76	16 <td>US-10-437-963-154283<td>Sequence 154283, A</td></td>	US-10-437-963-154283 <td>Sequence 154283, A</td>	Sequence 154283, A
25	40	57.1	260	12 <td>US-10-282-122A-65782<td>Sequence 65782, A</td></td>	US-10-282-122A-65782 <td>Sequence 65782, A</td>	Sequence 65782, A
26	40	57.1	261	12 <td>US-10-282-122A-65358<td>Sequence 65358, A</td></td>	US-10-282-122A-65358 <td>Sequence 65358, A</td>	Sequence 65358, A
27	40	57.1	333	16 <td>US-10-408-765A-241<td>Sequence 241, Appl</td></td>	US-10-408-765A-241 <td>Sequence 241, Appl</td>	Sequence 241, Appl
28	40	57.1	339	14 <td>US-10-156-761-8110<td>Sequence 8110, Appl</td></td>	US-10-156-761-8110 <td>Sequence 8110, Appl</td>	Sequence 8110, Appl
29	40	57.1	567	16 <td>US-10-389-566-2080<td>Sequence 2080, Appl</td></td>	US-10-389-566-2080 <td>Sequence 2080, Appl</td>	Sequence 2080, Appl
30	40	57.1	567	16 <td>US-10-389-566-2081<td>Sequence 2081, Appl</td></td>	US-10-389-566-2081 <td>Sequence 2081, Appl</td>	Sequence 2081, Appl
31	40	57.1	655	16 <td>US-10-389-566-2432<td>Sequence 2432, Appl</td></td>	US-10-389-566-2432 <td>Sequence 2432, Appl</td>	Sequence 2432, Appl
32	40	57.1	662	16 <td>US-10-389-566-789<td>Sequence 789, Appl</td></td>	US-10-389-566-789 <td>Sequence 789, Appl</td>	Sequence 789, Appl
33	40	57.1	662	16 <td>US-10-389-566-1436<td>Sequence 1436, Appl</td></td>	US-10-389-566-1436 <td>Sequence 1436, Appl</td>	Sequence 1436, Appl
34	40	57.1	669	16 <td>US-10-389-566-788<td>Sequence 788, Appl</td></td>	US-10-389-566-788 <td>Sequence 788, Appl</td>	Sequence 788, Appl
35	40	57.1	673	15 <td>US-10-409-701-21<td>Sequence 701, Appl</td></td>	US-10-409-701-21 <td>Sequence 701, Appl</td>	Sequence 701, Appl
36	40	57.1	673	16 <td>US-10-389-566-482<td>Sequence 482, Appl</td></td>	US-10-389-566-482 <td>Sequence 482, Appl</td>	Sequence 482, Appl
37	39	55.7	147	16 <td>US-10-437-963-14461<td>Sequence 14461, A</td></td>	US-10-437-963-14461 <td>Sequence 14461, A</td>	Sequence 14461, A
38	39	55.7	158	16 <td>US-10-437-963-192534<td>Sequence 192534, A</td></td>	US-10-437-963-192534 <td>Sequence 192534, A</td>	Sequence 192534, A
39	39	55.7	182	16 <td>US-10-437-963-113853<td>Sequence 113853, A</td></td>	US-10-437-963-113853 <td>Sequence 113853, A</td>	Sequence 113853, A
40	39	55.7	202	12 <td>US-10-282-122A-47701<td>Sequence 47701, A</td></td>	US-10-282-122A-47701 <td>Sequence 47701, A</td>	Sequence 47701, A
41	39	55.7	581	15 <td>US-10-369-493-9952<td>Sequence 9952, Appl</td></td>	US-10-369-493-9952 <td>Sequence 9952, Appl</td>	Sequence 9952, Appl
42	39	55.7	1016	16 <td>US-10-437-963-126592<td>Sequence 126592, A</td></td>	US-10-437-963-126592 <td>Sequence 126592, A</td>	Sequence 126592, A
43	39	55.7	103	16 <td>US-10-437-963-142339<td>Sequence 142339, A</td></td>	US-10-437-963-142339 <td>Sequence 142339, A</td>	Sequence 142339, A
44	38	54.3	135	12 <td>US-10-424-599-230499<td>Sequence 230499, A</td></td>	US-10-424-599-230499 <td>Sequence 230499, A</td>	Sequence 230499, A
45	38	54.3	139	14 <td>US-10-156-761-10961<td>Sequence 10961, A</td></td>	US-10-156-761-10961 <td>Sequence 10961, A</td>	Sequence 10961, A

ALIGNMENTS

US-10-169-297-49

Sequence 49, Application US/10169297

Publication No. US2003011276A1

GENERAL INFORMATION:

APPLICANT: Torodon, Naoki

APPLICANT: Murata, Masashi

APPLICANT: Enjoji, Takashi

TITLE OF INVENTION: Preventives and Remedies for Chronic

TITLE OF INVENTION: Hepatitis

FILE REFERENCE: 3435, 1000-000

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US/10/169, 297

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: JP 11/374087

PRIOR FILING DATE: 1999-12-28

NUMBER OF SEQ. ID NOS: 50

SOFTWARE: FastSeq for Windows Version 4.0

SEQ. ID NO. 49

LENGTH: 359

TYPE: PRT

ORGANISM: Homo sapiens

US-10-169-297-49

Query Match 100.0%; Score 70; DB 14; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ARRAVWCAVGE 13

DB 114 ARRAVWCAVGE 126

RESULT 2

US-10-076-816-4

Sequence 4, Application US/10076816

Publication No. US2003005624A1

```
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
APPLICANT: Hagie, Frank E.
TITLE OF INVENTION: Feed Additive Compositions and Methods
FILE REFERENCE: 50665-8021.US00
CURRENT APPLICATION NUMBER: US/10/076,816
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PR
ORGANISM: Homo sapiens
US-10-076-816-4
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```
Query Match 100.0%; Score 70; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ARRAVWCAVGE 13
DB 339 ARRAVWCAVGE 351
```

```
RESULT 3
US-10-077-381-4
Sequence 4, Application US/10077381
Publication No. US20030074700A1
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
APPLICANT: Hagie, Frank E.
TITLE OF INVENTION: Expression of Human Milk Proteins in
FILE REFERENCE: 50665-8022.US00
CURRENT APPLICATION NUMBER: US/10/077,381
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,199
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PR
ORGANISM: Homo sapiens
US-10-077-381-4
```

```
Query Match 100.0%; Score 70; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ARRAVWCAVGE 13
DB 339 ARRAVWCAVGE 351
```

```
RESULT 4
US-10-639-835-4
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```
Sequence 4, Application US/10639835
Publication No. US20040111766A1
GENERAL INFORMATION:
APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
APPLICANT: Hagie, Frank E.
TITLE OF INVENTION: Expression of Human Milk Proteins in
FILE REFERENCE: 50665-8022.US01
CURRENT APPLICATION NUMBER: US/10/639,835
PRIOR FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: US 10/077,381
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,199
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 690
TYPE: PR
ORGANISM: Homo sapiens
US-10-639-835-4
```

```
Query Match 100.0%; Score 70; DB 16; Length 690;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ARRAVWCAVGE 13
DB 339 ARRAVWCAVGE 351
```

```
RESULT 5
US-10-023-096-2
Sequence 2, Application US/10023096
Publication No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
City: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
```


REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-023-096-2

Query Match 100.0%; Score 70; DB 13; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVVMCAVGE 13
DB 343 ARARVVMCAVGE 355

RESULT 6
US-10-170-221-2
Sequence 2, Application US/10170221
Publication No. US20030192068A1
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/170,221
FILING DATE: 11-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-221-2

Query Match 100.0%; Score 70; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVVMCAVGE 13
DB 358 ARARVVMCAVGE 370

RESULT 7
US-10-169-297-9
Sequence 9, Application US/10169297
Publication No. US20030171276A1
GENERAL INFORMATION:
APPLICANT: Tomoda, Naoki
APPLICANT: Murata, Masashi
APPLICANT: Enjoji, Takashi
TITLE OF INVENTION: Preventives and Remedies for Chronic
Hepatitis
FILE REFERENCE: 3435, 1000-000
CURRENT APPLICATION NUMBER: US/10/169,297
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: PCT/JP00/09393
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 11/374087
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-169-297-9

Query Match 100.0%; Score 70; DB 14; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVVMCAVGE 13
DB 360 ARARVVMCAVGE 372

RESULT 8
US-10-170-221-4
Sequence 4, Application US/10170221
Publication No. US20030192068A1
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/170,221
  FILING DATE: 11-Jun-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/476,798
  FILING DATE: 07-JUN-1995
  APPLICATION NUMBER: US 08/077,788
  FILING DATE: 15-JUN-1993
  APPLICATION NUMBER: US 07/895,956
  FILING DATE: 15-JUN-1992
  APPLICATION NUMBER: US 07/619,131
  FILING DATE: 27-NOV-1990
  APPLICATION NUMBER: US 07/444,745
  FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
  NAME: Liebeschultz, Joe O.
  REGISTRATION NUMBER: 37,505
  REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-543-5043
  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 711 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-170-221-4

Query Match      100.0%; Score 70; DB 14; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
DB 360 ARARVWCAGE 372

RESULT 9
US-10-341-434-202
; Sequence 202, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent version 3.1
; SEQ ID NO 202
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-202

Query Match      100.0%; Score 70; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
DB 360 ARARVWCAGE 372
```

```

RESULT 10
US-10-341-434-218
; Sequence 218, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patent version 3.1
; SEQ ID NO 218
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-218

Query Match      100.0%; Score 70; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
DB 360 ARARVWCAGE 372

RESULT 11
US-10-440-464-69
; Sequence 69, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 69
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-69

Query Match      100.0%; Score 70; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
DB 360 ARARVWCAGE 372
```

RESULT 12

US-10-408-765A-2000
; Sequence 2000, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2000
; LENGTH: 711
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-408-765A-2000

Query Match

Best Local Similarity 100.0%; Score 70; DB 16; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAG 13

Db 360 ARARVWCAG 372

RESULT 13

US-10-169-297-35
; Sequence 35, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
; APPLICANT: Tohdoh, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; TITLE OF INVENTION: Hepatitis
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/JP00/09393
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 11/374087
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 234
; TYPE: PR1
; ORGANISM: Bos taurus
US-10-169-297-35

Query Match

Best Local Similarity 77.1%; Score 54; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12

Db 71 ARTRVWCAG 82

RESULT 14

US-10-169-297-8
; Sequence 8, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:

APPLICANT: Tohdoh, Naoki

APPLICANT: Murata, Masashi
APPLICANT: Enjoji, Takashi

TITLE OF INVENTION: Preventives and Remedies for Chronic
TITLE OF INVENTION: Hepatitis

FILE REFERENCE: 3435.1000-000
CURRENT APPLICATION NUMBER: US/10/169,297

CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: PCT/JP00/09393

PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 11/374087

PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8

LENGTH: 708
TYPE: PR1

ORGANISM: Bos taurus
US-10-169-297-8

Query Match 77.1%; Score 54; DB 14; Length 708;
Best Local Similarity 83.3%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAG 12

Db 359 ARTRVWCAG 370

RESULT 15

US-09-738-626-3901
; Sequence 3901, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3901
; LENGTH: 77
; TYPE: PR1
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3901

Query Match

Best Local Similarity 65.7%; Score 46; DB 9; Length 77;
Best Local Similarity 72.7%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRARVWCAG 12

Db 29 RRLRTWCAG 39

Search completed: September 1, 2004, 00:49:19
Job time : 30.64 secs

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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:03:45 ; Search time 7.54 Seconds

(without alignments)
165.847 Million cell updates/sec

Title: US-09-508-095-16

Perfect score: 70

Sequence: 1 ARRARVWCAVGE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78:*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	711	1	TFHUL
2	58	82.9	703	1	lactotransferrin p
3	54	77.1	708	1	lactotransferrin p
4	55	75.7	708	2	lactotransferrin p
5	52	74.3	707	1	lactotransferrin p
6	46	65.7	704	2	lactotransferrin p
7	44	62.9	705	1	lactotransferrin p
8	43	61.4	383	2	lactotransferrin p
9	42	60.0	1099	2	lactotransferrin p
10	40	57.1	260	2	lactotransferrin p
11	40	57.1	436	2	lactotransferrin p
12	40	57.1	483	2	lactotransferrin p
13	40	57.1	509	2	lactotransferrin p
14	40	57.1	562	2	lactotransferrin p
15	39.5	56.4	129	2	lactotransferrin p
16	39	55.7	285	1	lactotransferrin p
17	39	55.7	285	1	lactotransferrin p
18	39	55.7	350	2	lactotransferrin p
19	39	55.7	491	2	lactotransferrin p
20	39	55.7	549	2	lactotransferrin p
21	38	54.3	126	2	lactotransferrin p
22	38	54.3	150	2	lactotransferrin p
23	38	54.3	302	2	lactotransferrin p
24	38	54.3	326	2	lactotransferrin p
25	38	54.3	330	2	lactotransferrin p
26	38	54.3	337	2	lactotransferrin p
27	38	54.3	373	2	lactotransferrin p
28	38	54.3	386	2	lactotransferrin p
29	38	54.3	419	1	lactotransferrin p

ALIGNMENTS

30	38	54.3	437	2	B82778	cell cycle protein
31	38	54.3	505	2	B81021	conserved hypotet
32	38	54.3	505	2	C81965	hypothetical pepid
33	38	54.3	609	2	AB3031	conserved hypotet
34	38	54.3	765	2	B98254	hypothetical prote
35	38	54.3	870	2	T39731	csx2 protein - fls
36	37.5	53.6	199	2	A33653	tubulin alpha cha
37	37	52.9	176	2	F72563	hypothetical prote
38	37	52.9	203	2	JC7521	ribosomal protein
39	37	52.9	307	2	AE3466	malose transport
40	37	52.9	337	2	D72690	hypothetical prote
41	37	52.9	483	2	F83405	probable lyase PA3
42	37	52.9	706	2	S33761	transferrin precu
43	37	52.9	973	2	AB2340	hypothetical prote
44	36	51.4	108	2	F72507	hypothetical prote
45	36	51.4	134	2	T45188	hypothetical prote

RESULT 1

TFHUL

lactotransferrin precursor [validated] - human

N/Alternate names: lactoferrin

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text change 08-Dec-2000

C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R/Cho: Y.

submitted to the EMBL Data Library, March 1994

A/Reference number: G06820

A/Accession: G01394

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-711 <CHO>

A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AA60324.1; PID:G467237

R/Rev: M.W.; Moloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5289, 1990

A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A/Reference number: S11228; PMID:90384839; PMID:2402455

A/Accession: S11228

A/Molecule type: mRNA

A/Residues: 1-148; 'T', 150-422; 'C', 424-711 <REV>

A/Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R/Teng: C.T.; Liu, Y.; Yang, N.; Malmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A/Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A/Reference number: A45401; PMID:93125571; PMID:1480183

A/Accession: A45401

A/Molecule type: DNA

A/Residues: 1-15 <TEN>

A/Cross-references: GB:S52659; NID:G263311; PIDN:AA624877.1; PID:G263312

A/Experimental source: placenta

A/Note: sequence extracted from NCBI backbone (NCBIP:122202)

R/Powell, M.J.; Ogden, J.E.

Nucleic Acids Res. 18, 4013, 1990

A/Title: Nucleotide sequence of human lactoferrin cDNA.

A/Reference number: S10324; PMID:90326549; PMID:2274734

A/Accession: S10324

A/Molecule type: mRNA

A/Residues: 3-711 <POW>

A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedle, J.W.

Biochem. J. 276, 349-355, 1991

A/Title: Expression of cloned human lactoferrin in baby hamster kidney cells.

A/Reference number: S15853; PMID:91264786; PMID:2049066

A/Accession: S15853

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 20-31 <ST1>

A/Accession: S20841

A/Molecule type: protein

A/Residues: 20-28; 'X', 30-31 <ST2>

R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of MR
 A:Reference number: S07160; MUID:88001031; PMID:3477300
 A:Accession: S07160
 A:Molecule type: mRNA
 A:Residues: 435-487, 'A', 489-711 <RAD>
 A:Cross-references: EMBL:M16642; NID:9186815; PIDN:AAA86665.1; PID:G386855
 R:Parrella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; MUID:91235214; PMID:1674448
 A:Accession: A61169
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 3-701, 'SWKPVN' <PAN>
 A:Experimental source: normal breast tissue
 R:Metz-Poutigne, M.H.; Jollès, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1996
 A:Title: Human lactotransferrin amino acid sequence and structural comparisons with oth
 A:Reference number: A31000; MUID:85076687; PMID:85104420
 A:Accession: A31000
 A:Molecule type: Protein
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A:Note: this is the final paper in a series
 R:Hohen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affini
 A:Reference number: S74119; MUID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: Protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A:Experimental source: neutrophil granulocytes
 A:Gene: GDB:119368; OMIM:150210
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-71/Domain: signal sequence #status predicted <SIG>
 F:20-71/Product: lactotransferrin #status experimental <MAT>
 F:21-316/Domain: transferrin repeat homology <TRH1>
 F:360-699/Domain: transferrin repeat homology <TRH2>
 F:29-65, 39-56, 135-218, 177-193, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat

Query Match 100.0%; Score 70; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARPARVWCAYG 13
 DB 360 ARPARVWCAYG 372

RESULT 2
 A45543
 A:Title: Lactoferrin precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 04-Mar-2000
 C:Accession: A45543; S24173
 R:Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A:Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A:Reference number: A45543; MUID:92367939; PMID:1503259
 A:Accession: A45543
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-703 <ALB>
 A:Experimental source: mammary gland
 A:Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:111153)
 R:Lyden, J.P.; O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Conneely, O.M.

Biochim. Biophys. Acta 1132, 97-99, 1992
 A:Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A:Reference number: S24173; MUID:92379101; PMID:1511016
 A:Accession: S24173
 A:Molecule type: mRNA
 A:Residues: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
 A:Cross-references: EMBL:M92089; NID:G164613; PIDN:AAA1102.1; PID:G164614
 A:Experimental source: mammary gland
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-703/Product: lactoferrin #status predicted <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH1>
 F:36-48/Region: antimicrobial
 F:354-691/Domain: transferrin repeat homology <TRH2>
 F:38-62, 38-53, 129-212, 171-187, 184-195, 245-253, 362-384, 372-385, 419-698, 439-661, 471-546, 49
 F:77, 107, 206, 267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:335/Binding site: carbonate (Arg) #status predicted
 F:409, 447, 540, 609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:590/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.9%; Score 58; DB 2; Length 703;
 Best Local Similarity 83.3%; Pred. No. 0.021;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARPARVWCAYG 12
 DB 354 ARPARVWCAYG 365

RESULT 3
 TFBOL
 A:Title: Lactotransferrin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 11-May-2000
 C:Accession: I45919; S14674; S14110; S18517; J05095; S13097; S18518; S13881; PLO148; S21
 R:Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A:Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein fro
 A:Reference number: I45919
 A:Accession: I45919
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-708 <TSA>
 A:Cross-references: GB:I08604; NID:G163269; PIDN:AAA30609.1; PID:G163270
 R:Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S14674
 A:Accession: S14674
 A:Molecule type: mRNA
 A:Residues: 1-144, 'V', 146-163, 'PP', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI1>
 A:Cross-references: EMBL:X57084; NID:9505; PIDN:CAA40366.1; PID:9506
 R:Pierce, A.; Colavizza, D.; Benaisa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A:Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A:Reference number: S14110; MUID:91160550; PMID:2001696
 A:Accession: S14110
 A:Molecule type: mRNA
 A:Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A:Cross-references: EMBL:X57084
 A:Accession: S18517/
 A:Molecule type: Protein
 A:Residues: 20-35, 82-114, 148-163, 'PP', 166-178, 'V', 'P', 183-190, 205-212, 230-239, 304-339, 59
 R:Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A:Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glan
 A:Reference number: J05095; MUID:92028986; PMID:1718281
 A:Accession: J05095
 A:Molecule type: mRNA
 A:Residues: 1-65, 'PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A:Cross-references: GB:M63502

A>Note: The authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 R.Mead, P.E.; Tweedle, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A>Title: cDNA and protein sequence of bovine lactoferrin.
 A:Reference number: S13097; MUID:91088328; PMID:2263492
 A:Accession: S13097
 A:Molecule type: mRNA
 A:Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A:Cross-references: EMBL:X54801
 A:Accession: S18518
 A:Molecule type: protein
 A:Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586,587-589;598-619
 R.Mead, P.E.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S13881
 A:Accession: S13881
 A:Molecule type: mRNA
 A:Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
 A:Cross-references: EMBL:X54801
 R.Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A>Title: Purification and characterization of bovine lactoferrin from secretions of the
 A:Reference number: P10148; MUID:90031466; PMID:2805645
 A:Accession: P10148
 A:Molecule type: protein
 A:Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R.Bellamy, W.; Takase, M.; Yamauchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A>Title: Identification of the bactericidal domain of lactoferrin.
 A:Reference number: S21756; MUID:92287941; PMID:1599934
 A:Accession: S21756
 A:Molecule type: protein
 A:Residues: 36-60 <BEL>
 R.Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A>Title: Separation and characterization of the C-terminal half molecule of bovine lacto
 A:Reference number: A56659; MUID:93253156; PMID:8486845
 A:Accession: A56659
 A:Molecule type: protein
 A:Residues: 20-25;302-308;359-366, 'X', 368-376, 'X', 378 <SHI>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-708/Product: lactotransferrin #status experimental <MAT>
 F:20-355/Domains: transferrin repeat homology <TRH1>
 F:36-60/Region: antimicrobial
 F:359-696/Domains: transferrin repeat homology <TRH2>
 F:28-64;134-217, 176-192, 179-200,189-202,250-264,367-399,377-390,424-703,444-666,476-551,
 F:38-55/Disulfide bonds: #status predicted
 F:79,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:140/Binding site: carbonate (Arg) #status experimental
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:414,452,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:482/Binding site: carbonate (Arg) #status experimental

Query Match 77.1%; Score 54; DB 1; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 12
 |||
 DB 359 ARTRVWCAVG 370

RESULT 4
 JUC2323
 lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JUC2323
 R:Je Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus

A:Reference number: JUC2323; MUID:94380047; PMID:8093048
 A:Accession: JUC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:358-696/Domains: transferrin repeat homology <TRH2>
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.7%; Score 53; DB 2; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.16;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 12
 |||
 DB 359 ARTRVWCAVG 370

RESULT 5
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280035; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R.Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domains: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domains: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.3%; Score 52; DB 1; Length 707;
 Best Local Similarity 75.0%; Pred. No. 0.24;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 12
 |||
 DB 358 ASKARVWCAVG 369

RESULT 6
 I47228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
 C:Accession: I47228
 R:Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from por
 A:Reference number: I47228; MUID:93099129; PMID:1463741
 A:Accession: I47228
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-704 <ROU>
 A:Cross-references: EMBL:U36916; NID:G1016329; PIDN:AAB58956.1; PID:G1016330
 C:Genetics:

A:Gene: PICA
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication
F:20-350/Domain: transferrin repeat homology <TRH1>
Query Match 65.7%; Score 46; DB 2; Length 704;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CY 5 RYVMCAVGE 13
DB 356 RYVMCAVGO 364
RESULT 7
TPOCHE
M:Alternate names: conalbumin; transferrin
C:Species: Gallus gallus (chicken)
C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: A26845; A91115; A92229; A91116; A40674; B61573; A90282; S02476; A03262
R:Jeltsch, J.M.; Hen, R.; Marcoteaux, L.; Garnier, J.M.; Chambon, P.
Nucleic Acids Res. 15, 7643-7645, 1987
A>Title: Sequence of the chicken ovotransferrin gene.
A:Reference number: A26845; MUID:88015626; PMID:3658709
A:Accession: A26845
A:Molecule type: DNA
A:Residues: 1-705 <JE1>
A:Cross-references: GB:Y00407; NID:963131; PIDN:CA68468.1; PID:G295721
R:Jeltsch, J.M.; Chambon, P.
Eur. J. Biochem. 122, 291-295, 1982
A>Title: The complete nucleotide sequence of the chicken ovotransferrin mRNA.
A:Reference number: A91115; MUID:82138851; PMID:7060577
A:Accession: A91115
A:Molecule type: mRNA
A:Residues: 1-82, 'V', 84-99, 'I', 101-153, 'W', 155-238, 'LN', 241-685, 'N', 687-705 <JE2>
A:Cross-references: EMBL:X02009
A>Note: the codons given for residues 132 (AAC) and 317 (UUC) are inconsistent with the
R:Thibodeau, S.N.; Lee, D.C.; Palmiter, R.D.
J. Biol. Chem. 253, 3771-3774, 1978
A>Title: Identical precursors for serum transferrin and egg white conalbumin.
A:Reference number: A92229; MUID:78171533; PMID:649604
A:Accession: A92229
A:Molecule type: protein
A:Residues: 1-23 <TH1>
R:Williams, J.; Ellerman, T.C.; Kingston, I.B.; Wilkins, A.G.; Kuhn, K.A.
Eur. J. Biochem. 122, 297-303, 1982
A>Title: The primary structure of hen ovotransferrin.
A:Reference number: A91116; MUID:82138852; PMID:6895872
A:Accession: A91116
A:Molecule type: protein
A:Residues: 1-56; 54-82, 'V', 84-92; 102-146; 162-168; 170-228; 241-263; 289-333; 338-344; 350-351
R:Gentili, C.; Bianco, P.; Neri, M.; Malpell, M.; Campanile, G.; Castagnola, P.; Cancedo
J. Cell Biol. 122, 703-712, 1993
A>Title: Cell proliferation, extracellular matrix mineralization, and ovotransferrin tra
A:Reference number: A40674; MUID:93328771; PMID:8393014
A:Accession: A40674
A:Molecule type: protein
A:Residues: 20-28, 'X', 30-38, 'X', 40-44 <GEN>
R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: B61573
A:Molecule type: protein
A:Residues: 20-28, 'X', 30-38, 'X', 40-43, 'S' <CHD>
R:Kingston, I.B.; Williams, J.
Biochem. J. 147, 463-472, 1975
A>Title: The amino acid sequence of a carbohydrate-containing fragment of hen ovotransfe
A:Reference number: A90282; MUID:76039467; PMID:1172663
A:Accession: A90282
A:Molecule type: protein

A:Residues: 480-582 <KIN>
R:Ellerman, T.C.; Williams, J.
Biochem. J. 116, 515-532, 1970
A>Title: The amino acid sequences of cysteine acid-containing peptides from performic acid
A:Reference number: A90246; MUID:70141846; PMID:4907959
A:Contents: annotation; disulfide bonds
R:Williams, J.; Moreton, K.
Biochem. J. 251, 849-855, 1988
A>Title: The dimerization of half-molecule fragments of transferrin.
A:Reference number: S02476; MUID:88326225; PMID:3415649
A:Accession: S02476
A:Molecule type: protein
A:Residues: 20-23; 295-302; 336-366; 674-679, 'T', 681, 'F', 683-685, 'N', 687-705 <M12>
C:Comment: Ovotransferrin (conalbumin) and transferrin have identical protein components
xrin is synthesized in the liver.
C:Comment: Ovotransferrin has a bacteriostatic function. Its concentration in avian egg v
C:Comment: Plasma apotransferrin promotes the oxidation of ferrous ions, which would othe
C:Comment: In electrophoretic and genetic studies, transferrin shows strong polymorphism,
C:Genetics:
A:Mutations: 15/1; 69/3; 106/1; 170/1; 215/2; 234/1; 290/3; 353/1; 404/3; 436/1; 448/1; 500
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; egg white; glycoprotein; iron binding; plasma
F:1-19/Domain: signal sequence #status experimental <SIG>
F:120-705/Product: transferrin #status experimental <WAT>
F:21-355/Domain: transferrin repeat homology <TRH1>
F:359-692/Domain: transferrin repeat homology <TRH2>
F:29-64; 134-216; 179-193; 190-201; 247-261; 367-399; 424-699; 440-662; 473-549; 497-690/Disulfide
F:35-55; 377-390; 589-603/Disulfide bonds: #status predicted
F:492/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F:507-521; 518-532/Disulfide bonds: (or 507-518, 521-532) #status predicted
Query Match 62.9%; Score 44; DB 1; Length 705;
Best Local Similarity 58.3%; Pred. No. 6.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CY 2 RRYVMCAVGE 13
DB 360 RRRIGCAVGR 371
RESULT 8
succinyl-diaminopimelate desuccinylase PA1162 [imported] - Pseudomonas aeruginosa (strain
G83500
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83500
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardis, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83500
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:AE004546; GB:AE004091; NID:99947079; PIDN:AA04551.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: dape, PA1162
C:Superfamily: succinyl-diaminopimelate desuccinylase
Query Match 61.4%; Score 43; DB 2; Length 383;
Best Local Similarity 61.5%; Pred. No. 5.5;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CY 1 ARRYVMCAVGE 13
DB 158 ARGERLDWCVGE 170
RESULT 9
A59311

C:Keywords: glycosidase; hydrolase

Query Match 57.1%; Score 40; DB 2; Length 509;
 Best Local Similarity 61.5%; Pred. No. 24;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ARARVWCAYGE 13
 ||:||||
 DB 248 AKRRVLMGWGE 260

RESULT 14

JC7906

sucrose 1F-fructosyltransferase (EC 2.4.1.99) - wheat
 N:Alternate names: 1-SST; fructosyltransferase 2; wft2 protein
 C:Species: Triticum aestivum (common wheat)

C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 14-Apr-2003

C:Accession: JC7906

R:Kawakami, A.; Yoshida, M.

Biosci. Biotechnol. Biochem. 66, 2297-2305, 2002

A:Title: Molecular characterization of sucrose:sucrose 1-fructosyltransferase and sucrose

A:Reference number: JC7905; MUID:22394650; PMID:12506964

A:Accession: JC7906

A:Molecule type: mRNA

A:Residues: 1-662 <KAN>

A:Cross-references: DDBJ:AB029888

C:Comment: This enzyme, which is a vacuole-type fructosyltransferase and a fructan-biosy

C:Genetics: fers a fructosyl moiety from one sucrose to another, resulting in the formation of trise

A:Gene: wft2

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 57.1%; Score 40; DB 2; Length 662;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 RRARVWCAYGE 13
 ::|||||
 DB 402 KRRVWYAYGE 413

RESULT 15

C87219

hypothetical protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: C87219

R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltham, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: C87219

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <STO>

A:Cross-references: GB:ALA50380; NID:q13094034; PIDN:CAC31395.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML2478

Query Match 56.4%; Score 39.5; DB 2; Length 129;
 Best Local Similarity 60.0%; Pred. No. 8.7;
 Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

OY 1 ARR--ARVWCAYG 12
 ||| ||| ||| |||
 DB 51 ARRVDFARASCWVG 65

Search completed: September 1, 2004, 00:17:01
 Job time : 8.54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:44 ; Search time 4.42 Seconds
(without alignments)
153.148 Million cell updates/sec

Title: US-09-508-095-16

Perfect score: 70

Sequence: 1 ARRAVWCAVGE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	711	1	TRFL_HUMAN
2	65	92.9	708	1	TRFL_BUBBU
3	60	85.7	695	1	TRFL_HORSE
4	58	82.9	704	1	TRFL_PIG
5	57	81.4	708	1	TRFL_CAMDR
6	54	77.1	708	1	TRFL_BOVIN
7	53	75.7	708	1	TRFL_CAPHI
8	52	74.3	707	1	TRFL_MOUSE
9	46	63.7	704	1	ICA_FIG
10	44	62.9	705	1	TRFE_CHICK
11	41	58.6	686	1	TRFE_ANAPL
12	39	55.7	285	1	REP2_ECOLI
13	38	54.3	870	1	CSX2_SCHPO
14	37	52.9	176	1	YH92_AERPE
15	37	52.9	705	1	TRFE_HORSE
16	36	51.4	328	1	CAHB_HUMAN
17	36	51.4	375	1	DAPE_ECOLI
18	36	51.4	377	1	DAPE_HAEIN
19	36	51.4	449	1	CI3A_MYCTU
20	36	51.4	696	1	TRFE_PIG
21	36	51.4	1935	1	ATG9_HUMAN
22	35	50.0	174	1	YH11_MYCTU
23	35	50.0	188	1	Y768_AQUAE
24	35	50.0	220	1	Y231_RICPR
25	35	50.0	502	1	Y22R_AGRVI
26	35	50.0	642	1	TRFE_GADMO
27	35	50.0	687	1	TRFE_ONCKI
28	35	50.0	690	1	TRFE_SALSA
29	35	50.0	690	1	TRFE_ORYLA
30	35	50.0	691	1	TRFE_SALSA
31	35	50.0	697	1	TRFE_MOUSE
32	35	50.0	698	1	TRFE_RAT
33	35	50.0	704	1	TRFE_BOVIN

34	35	50.0	771	1	RIRI_VACC	P20503 vaccinia vi
35	35	50.0	771	1	RIRI_VACCV	P12848 vaccinia vi
36	35	50.0	771	1	RIRI_VARV	P32984 variola vir
37	35	50.0	895	1	GNDS_RAT	O03586 rattus norv
38	35	50.0	914	1	GNDS_HUMAN	O12567 homo sapien
39	35	50.0	1333	1	PAD3_MOUSE	O99h2 mus musculu
40	35	50.0	1337	1	PAD3_RAT	O92340 rattus norv
41	35	50.0	2663	1	CENE_HUMAN	O02224 homo sapien
42	34	48.6	81	1	YGS4_PASMT	O9CK94 pasteurella
43	34	48.6	125	1	YBUN_ECOLI	P75813 escherichia
44	34	48.6	166	1	CSGA_MTXKA	P21158 myxococcus
45	34	48.6	239	1	6PGL_XYLFA	O9pe95 xylella fas

ALIGNMENTS

```

RESULT 1
ID      TRFL_HUMAN      STANDARD;          PRT;      711 AA.
AC      P02788; O00756; Q16780; Q16785; Q16786; Q16789; Q96KZ4; Q96KZ5;
AC      O9H123;
DT      21-JUN-1986 (Rel. 01, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Lactoferrin precursor (lactoferrin) [Contains: Lactoferrin A;
GN      LRF OR LF.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RX      MEDLINE=90364839; PubMed=2402455;
RA      Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT      "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL      Nucleic Acids Res. 18:5288-5288(1990).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RA      Cho Y.Y.;
RT      Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      Submitted (XAY-1992) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RA      Liang Q., Jimenez-Flores R., Richardson T.;
RT      "Molecular cloning and sequence analysis of human lactoferrin.";
RN      Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Bone marrow;
RA      Wei X., Han J., Rado T.A.;
RT      "Human neutrophil lactoferrin coding and 5' flanking region DNA
sequences.";
RN      Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN      [6]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RA      Cheng H., Chen X., Huan L.;
RT      "cDNA cloning and sequence analysis of human lactoferrin.";
RN      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN      [7]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Prostate;
RA      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

```

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA";
RT Nucleic Acids Res. 18:4013-4013 (1990).
RN [9]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Met-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legend D., Spik G., Montreuil J., Jolles P.;
RT "Human lactotransferrin: amino acid sequence and structural
RT comparisons with other transferrins";
RT Eur. J. Biochem. 145:659-666 (1984).
RN [10]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
RX MEDLINE=82046817; PubMed=6794640;
RA Met-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactotransferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of
RT N- and C-terminal domains";
RT Biochim. Biophys. Acta 670:243-254 (1981).
RN [11]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727;
RA Met-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactotransferrin";
RT FEBS Lett. 142:107-110 (1982).
RN [12]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis";
RT Blood 70:989-993 (1987).
RN [13]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombe W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Madis E., Schurz D.,
RA Ghoi L., Ia Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Drazan V., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagipanti J.,
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=258506;
RA Anderson B.F., Baker H.M., Norris G.B., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution";

RT J. Mol. Biol. 209:711-734 (1989).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human lactoferrin refined at 2.2-A
RT resolution";
RT Acta Crystallogr. D 51:629-646 (1995).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253->methionine mutant";
RT Biochemistry 36:341-346 (1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori";
RT Acta Crystallogr. D 55:403-407 (1999).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement
RT and analysis of ligand-induced conformational change";
RT Acta Crystallogr. D 54:1319-1335 (1998).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=91166929; PubMed=1369293;
RA Tani F., Ito K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of opioic antagonist peptides derived
RT from human lactoferrin";
RT Agric. Biol. Chem. 54:1803-1810 (1990).
RN [20]
RP VARIANTS THR-30 AND ARG-48.
RX MEDLINE=99091914; PubMed=9873069;
RA Kinsworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
RA Sugar J., Kumararamanickavel G., Munier F., Schoderet D.F.,
RA El-Matiri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
RA Hajtanack U.P., Teng C.T.;
RT "Familial subepithelial corneal amyloidosis (gelatinous drop-like
RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
RT Mol. Vision 4:31-32 (1998).
RN [21]
RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
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CC -----
CC DR EMBL; X53961; CAA37914.1; -
CC DR EMBL; U07643; AAB60324.1; -
CC DR EMBL; M93150; AAA36159.1; -
CC DR EMBL; M83202; AAA59511.1; -
CC DR EMBL; M83205; AAA58656.1; -

Query Match 100.0%; Score 70; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARYWCAYGE 13
DB 360 ARRARYWCAYGE 372

RESULT 2
TRFL_BUBBU STANDARD; PRT; 708 AA.
AC 07698;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactoferrin precursor (Lactoferrin).
GN LTP.
OS Bubalus bubalis (domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RA Paramasivam M., Thattaiyath B.D., Kumar A., Srinivasan A.,
RA Singh T.P.;
RT "CDNA sequence of Buffalo lactoferrin."
RL Submitted (JUN-1998) to the EMBL/GenBank/DDb databases.

RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=20003130; PubMed=10531476;
RA Karthikeyan S., Paramasivam M., Yadav S., Srinivasan A., Singh T.P.;
RT "Structure of buffalo lactoferrin at 2.5-A resolution using crystals
grown at 303 K shows different orientations of the N and C lobes."
RL Acta Crystallogr. D 55:1805-1813 (1999).

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: Composed of two homologous domains.
CC -!- SIMILARITY: Belongs to the transferrin family.

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CC EMBL; AJ005203; CA06441.1; -.
CC PDB; 1CB2; 19-MAR-99.
CC PDB; 1BIY; 13-JAN-99.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin; 2.
CC PRINTS; PRO0422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal; 3d-structure; 19

FT SIGNAL 1 19
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT DISULFID 28 64
FT DISULFID 38 55
FT DISULFID 134 217
FT DISULFID 176 192
FT DISULFID 179 202
FT DISULFID 189 200

FT DISULFID 250 264
FT DISULFID 367 390
FT DISULFID 377 399
FT DISULFID 424 703
FT DISULFID 444 666
FT DISULFID 476 581
FT DISULFID 500 694
FT DISULFID 510 524
FT DISULFID 521 534
FT DISULFID 592 606
FT DISULFID 644 649
FT METAL 79 79
FT METAL 111 111
FT METAL 211 211
FT METAL 272 272
FT METAL 414 414
FT METAL 452 452
FT METAL 545 545
FT METAL 614 614
FT BINDING 136 136
FT BINDING 140 140
FT BINDING 142 142
FT BINDING 143 143
FT BINDING 478 478
FT BINDING 482 482
FT BINDING 484 484
FT BINDING 485 485
FT CARBOHYD 252 252
FT CARBOHYD 300 300
FT CARBOHYD 495 495
FT TURN 564 564
FT TURN 21 22
FT STRAND 25 29
FT HELIX 32 46
FT TURN 47 48
FT STRAND 53 57
FT HELIX 61 69
FT TURN 70 71
FT STRAND 75 78
FT HELIX 80 87
FT TURN 89 91
FT STRAND 93 102
FT STRAND 107 108
FT STRAND 110 118
FT TURN 119 120
FT HELIX 125 127
FT TURN 129 130
FT STRAND 132 135
FT TURN 138 139
FT TURN 141 144
FT HELIX 145 150
FT TURN 151 151
FT HELIX 152 155
FT TURN 159 161
FT HELIX 164 169
FT TURN 170 171
FT STRAND 174 176
FT TURN 178 179
FT TURN 182 184
FT HELIX 186 189
FT TURN 190 191
FT HELIX 196 198
FT TURN 199 200
FT TURN 204 205
FT TURN 207 208
FT HELIX 211 219
FT TURN 220 221
FT STRAND 225 229
FT TURN 230 231
FT HELIX 232 236
FT HELIX 240 243
FT TURN 244 245
FT STRAND 246 249

IRON 1.
IRON 1.
IRON 1.
IRON 1.
IRON 2.
IRON 2.
IRON 2.
IRON 2.
CARBONATE 1.
CARBONATE 1.
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 2.
CARBONATE 2.
CARBONATE 2 (VIA AMIDE NITROGEN).
CARBONATE 2 (VIA AMIDE NITROGEN).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 92.9%; Score 65; DB 1; Length 708;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARARVWCavg 12

DB 359 ARARVWCavg 370

RESULT 3
 TRFL HORSE
 ID TRFL HORSE STANDARD; PRT; 695 AA.

AC 077811; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactoferrin precursor (lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CC NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=9928631; Pubmed=1036507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare dimeric lactoferrin at 2.6-A
 resolution";
 RL J. Mol. Biol. 289:303-317(1999).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.

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 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AJ010930; CAA09407.1; -
 DR PDB; 1BIX; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR PDB; 1F9S; 10-FEB-01.
 DR PDB; 116B; 13-FEB-02.
 DR PDB; 1QJW; 14-JAN-00.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KM Signal; 3D-structure.
 FT NON TER 1 1
 FT SIGNAL <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.
 FT DISULFID 15 51
 FT DISULFID 25 42
 FT DISULFID 121 204
 FT DISULFID 163 179
 FT DISULFID 166 189
 FT DISULFID 176 187
 FT DISULFID 237 251

FT DISULFID 354 386
FT DISULFID 364 377
FT DISULFID 411 680
FT DISULFID 431 653
FT DISULFID 463 538
FT DISULFID 487 681
FT DISULFID 497 511
FT DISULFID 508 521
FT DISULFID 579 583
FT DISULFID 631 636
FT METAL 66 66
FT METAL 98 98
FT METAL 198 198
FT METAL 259 259
FT METAL 401 401
FT METAL 439 439
FT METAL 532 532
FT METAL 601 601
FT BINDING 123 123
FT BINDING 127 127
FT BINDING 129 129
FT BINDING 130 130
FT BINDING 445 445
FT BINDING 469 469
FT BINDING 471 471
FT BINDING 472 472
FT CARBOHYD 143 143
FT CARBOHYD 287 287
FT CARBOHYD 482 482
FT STRAND 12 12
FT HELIX 19 34
FT TURN 35 36
FT STRAND 40 44
FT HELIX 48 56
FT TURN 57 58
FT STRAND 62 65
FT HELIX 67 74
FT TURN 76 78
FT STRAND 80 88
FT STRAND 95 95
FT STRAND 97 105
FT TURN 106 107
FT HELIX 112 114
FT TURN 116 117
FT STRAND 119 122
FT TURN 125 126
FT TURN 128 131
FT HELIX 132 137
FT HELIX 139 142
FT TURN 147 148
FT HELIX 151 158
FT STRAND 161 163
FT TURN 165 166
FT TURN 169 171
FT HELIX 173 175
FT TURN 176 178
FT TURN 183 187
FT TURN 191 192
FT TURN 194 195
FT HELIX 197 206
FT TURN 207 216
FT STRAND 212 216
FT HELIX 219 223
FT HELIX 227 230
FT TURN 231 232
FT STRAND 233 237
FT TURN 238 240
FT STRAND 241 244
FT HELIX 245 247
FT TURN 248 250
FT STRAND 254 257
FT STRAND 260 264
FT HELIX 284 284

IRON 1.
IRON 1.
IRON 1.
IRON 1.
IRON 2.
IRON 2.
IRON 2.
CARBONATE 1.
CARBONATE 1.
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 2.
CARBONATE 2.
CARBONATE 2 (VIA AMIDE NITROGEN).
CARBONATE 2 (VIA AMIDE NITROGEN).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT TURN 286 287
FT TURN 294 295
FT TURN 308 309
FT STRAND 312 315
FT HELIX 322 326
FT TURN 328 336
FT TURN 337 338
FT HELIX 341 349
FT STRAND 351 356
FT HELIX 358 370
FT TURN 371 372
FT STRAND 375 380
FT HELIX 383 392
FT TURN 393 393
FT STRAND 397 400
FT HELIX 402 410
FT TURN 411 412
FT STRAND 414 421
FT HELIX 429 433
FT STRAND 439 446
FT HELIX 454 456
FT TURN 458 459
FT STRAND 462 464
FT TURN 467 468
FT TURN 470 473
FT HELIX 474 484
FT HELIX 489 491
FT TURN 492 492
FT STRAND 496 497
FT TURN 499 500
FT TURN 503 504
FT TURN 506 507
FT STRAND 508 508
FT TURN 515 516
FT TURN 520 521
FT TURN 525 526
FT TURN 528 529
FT HELIX 531 540
FT TURN 541 542
FT STRAND 546 550
FT HELIX 551 555
FT TURN 556 557
FT TURN 559 560
FT HELIX 565 568
FT TURN 569 569
FT TURN 572 573
FT STRAND 575 578
FT TURN 580 581
FT STRAND 584 586
FT HELIX 587 592
FT STRAND 596 598
FT STRAND 602 605
FT TURN 607 609
FT HELIX 610 624
FT TURN 626 627
FT TURN 629 630
FT HELIX 631 634
FT TURN 637 638
FT TURN 641 642

Query Match 85.7%; Score 60; DB 1; Length 695;
Best Local Similarity 91.7%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPARVWCAGV 12
DB 346 ARRRVWCAGV 357

RESULT 4
ID TRFL_PIG STANDARD; PRT: 704 AA.
AC P14632; Q29557;

DT 01-APR-1990 (Rel. 14, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin).
 GN LTF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92379101; PubMed=1511016;
 RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Headon D.R.,
 RA Connolly O.M.;
 RT "Nucleotide and primary amino acid sequence of porcine lactoferrin";
 RL Biophys. Biophys. Acta 1132:97-99(1992).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92367939; PubMed=1503259;
 RA Alexander L.J., Levine W.B., Teng C.T., Beattie C.W.;
 RT "Cloning and sequencing of the porcine lactoferrin cDNA";
 RL Anim. Genet. 23:251-256(1992).
 RN (3)
 RP SEQUENCE OF 20-49.
 RX MEDLINE=90105338; PubMed=2605266;
 RA Hutchens T.W., Magnuson J.S., Yip T.-T.;
 RT "Rapid purification of porcine colostrum whey lactoferrin by affinity
 chromatography on single-stranded DNA-agarose. Characterization,
 amino acid composition and N-terminal amino acid sequence";
 RL Biophys. Biophys. Acta 999:323-329(1989).
 CC -1- FUNCTION: TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M92089; AAA1102.1; -.
 DR EMBL: M81327; AAA1059.1; -.
 DR PIR: A45543; A45543.
 DR HSP: O77696; 1CE2.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00442; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 DR Transprot; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 704 LACTOTRANSFERRIN.
 FT REPEAT 20 359
 FT REPEAT 360 704 1.
 FT DISULFID 28 62 BY SIMILARITY.
 FT DISULFID 38 53 BY SIMILARITY.
 FT DISULFID 130 213 BY SIMILARITY.
 FT DISULFID 172 188 BY SIMILARITY.
 FT DISULFID 185 196 BY SIMILARITY.
 FT DISULFID 246 260 BY SIMILARITY.
 FT DISULFID 363 395 BY SIMILARITY.
 FT DISULFID 373 386 BY SIMILARITY.
 FT DISULFID 420 699 BY SIMILARITY.
 FT DISULFID 472 547 BY SIMILARITY.

FT DISULFID 496 690 BY SIMILARITY.
 FT DISULFID 506 520 BY SIMILARITY.
 FT DISULFID 517 530 BY SIMILARITY.
 FT DISULFID 588 602 BY SIMILARITY.
 FT DISULFID 640 645 BY SIMILARITY.
 FT METAL 77 77 IRON 1 (BY SIMILARITY).
 FT METAL 107 107 IRON 1 (BY SIMILARITY).
 FT METAL 207 207 IRON 1 (BY SIMILARITY).
 FT METAL 268 268 IRON 1 (BY SIMILARITY).
 FT METAL 410 410 IRON 2 (BY SIMILARITY).
 FT METAL 448 448 IRON 2 (BY SIMILARITY).
 FT METAL 541 541 IRON 2 (BY SIMILARITY).
 FT METAL 610 610 IRON 2 (BY SIMILARITY).
 FT BINDING 132 132 CARBONATE 1 (BY SIMILARITY).
 FT BINDING 136 136 CARBONATE 1 (BY SIMILARITY).
 FT BINDING 138 138 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
 SIMILARITY).
 FT BINDING 139 139 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
 SIMILARITY).
 FT BINDING 474 474 CARBONATE 2 (BY SIMILARITY).
 FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
 FT BINDING 480 480 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
 SIMILARITY).
 FT BINDING 481 481 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
 SIMILARITY).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 491 491 G-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 12 12 G -> W (IN REF. 1).
 FT CONFLICT 46 46 RRT -> TTR (IN REF. 3).
 FT CONFLICT 51 51 M -> I (IN REF. 1).
 FT CONFLICT 85 85 D -> G (IN REF. 1).
 FT CONFLICT 121 121 MISSING (IN REF. 2).
 FT CONFLICT 132 132 T -> I (IN REF. 1).
 FT CONFLICT 133 132 E -> S (IN REF. 1).
 FT CONFLICT 284 284 E -> Q (IN REF. 1).
 FT CONFLICT 573 573 D -> N (IN REF. 1).
 FT CONFLICT 590 590 V -> M (IN REF. 1).
 FT CONFLICT 625 625 V -> C (IN REF. 1).
 FT CONFLICT 662 662 V -> C (IN REF. 1).
 FT CONFLICT 704 704 NLKQCSVPLTACAFMR -> T (IN REF. 1).
 SQ SEQUENCE 704 AA; 77625 MW; 93261EPD08AD358 CRC64;
 Query Match 82.9%; DB 1; Length 704;
 Best Local Similarity 83.3%; Pred. No. 0.0074;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARRRVWCavg 12
 DB 355 ARQKVCavg 366
 RESULT 5
 TRFL_CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUD0; Q9WZS5;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin).
 GN LTF.
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_TaxID=9838;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Small; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";
 RL Int. Dairy J. 9:481-486(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Sahani M.S., Singh T.P.;

Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

CC - FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).

CC - SUBUNIT: Monomer (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: Secreted.

CC - DOMAIN: Composed of two homologous domains.

CC - SIMILARITY: Belongs to the transferrin family.

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: AJ131674; CAB53387.1; -
CC EMBL: AF165879; AAF82241.1; -
CC PDB: 1DTZ; 20-JUN-01.
CC InterPro: IPR001156; Transferrin.
CC Pfam: PF00405; Transferrin; 2.
CC PRINTS: PR00422; TRANSFERRIN.
CC SMART: SMO0094; TR_FER; 2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.
CC PROSITE: PS00206; TRANSFERRIN_2; 2.
CC PROSITE: PS00207; TRANSFERRIN_3; 2.
CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal; 3D-structure.

KM Signal; 1 19 BY SIMILARITY.
KW CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 BY SIMILARITY.
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 136 136 CARBONATE 1 (BY SIMILARITY).
FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 143 143 SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
FT BINDING 478 478 SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (BY SIMILARITY).
FT BINDING 484 484 CARBONATE 2 (BY SIMILARITY).
FT BINDING 485 485 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
FT BINDING 485 485 SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).
FT CONFLICT 506 506 L -> F (IN REF. 2).
FT CONFLICT 609 609 A -> P (IN REF. 2).
FT CONFLICT 642 642 R -> Q (IN REF. 2).
SQ SEQUENCE 708 AA; 77211 MM; 0B0C175A0B65D430 CRC64;

Query Match 81.4%; Score 57; DB 1; Length 708;
Best Local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAVWCAVG 12
DB 360 RRAQVWCAVG 370

RESULT 6
TRFL BOVIN STANDARD; PRT; 708 AA.
AC P24627; Q29629; Q9WZ73.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [contains: Lactoferricin B
DE (LFCIN B)].
GN LTF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Supramaxillary gland;
RX MEDLINE=91160550; PubMed=2001696;
RA Pierce A., Colavizza D., Bernassa M., Maes P., Tartar A.,
RA Montreuil J., Spik G.;
RT "Molecular cloning and sequence analysis of bovine lactotransferrin";
RT Eur. J. Biochem. 196;177-184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92028986; PubMed=1718281;
RA Goodman R.E., Schanbacher F.L.;
RT "Bovine lactoferrin mRNA: sequence, analysis, and expression in the
RT mammary gland";
RT Biochem. Biophys. Res. Commun. 180;75-84(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Tsang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.W., Stern D.;
RT "Cloning of a 80-kD advanced glycosylation end product (AGE) binding
RT protein from bovine lung";
RT PNASB U. S. 6;233-233(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood; and Mammary gland;
RX MEDLINE=94266164; PubMed=8206385;
RA Seyfert H.-M., Tuckoritz A., Interthal H., Koczan D., Hobom G.;
RT "Structure of the bovine lactoferrin-encoding gene and its promoter";
RT Gene 143;265-269(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Nakamura T., Shimazaki K., Yagi Y., Watanabe A.;
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE OF 20-59.
RX MEDLINE=90031466; PubMed=2805645;
RA Rejman J.J., Hegarty H.M., Hurley M.L.;
RT "Purification and characterization of bovine lactoferrin from
RT secretions of the involuting mammary gland: identification of
RT multiple molecular weight forms";

FT TURN 196 197

Query Match 77.1%; Score 54; DB 1; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.039;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRARVWCAGV 12
 |||||
 Db 359 ARRYVWCAGV 370

RESULT 7
 TRFL_MOUSE STANDARD; PRT; 708 AA.

ID TRFL_MOUSE
 AC 029477; 029479; (Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U12 syntenic group."
 RL Biochem. Biophys. Res. Commun. 203:1324-1332(1994).
 CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC
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 CC
 CC EMBL: U53857; AAA97958.1; -
 CC EMBL: X78902; CA55517.1; -
 CC HSSP: O77698; ICE2.
 CC InterPro: IPR001156; Transferrin.
 CC Pfam: PF00405; transferrin; 2.
 CC PRINTS: PR00422; TRANSFERRIN.
 CC SMART: SM00094; TR_PFR; 2.
 CC PROSITE: PS00205; TRANSFERRIN_1; 2.
 CC PROSITE: PS00206; TRANSFERRIN_2; 2.
 CC PROSITE: PS00207; TRANSFERRIN_3; 2.
 CC Transprot: Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 708 LACTOTRANSFERRIN.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 BY SIMILARITY.
 FT DISULFID 38 55 BY SIMILARITY.
 FT DISULFID 134 217 BY SIMILARITY.

FT DISULFID 176 192 BY SIMILARITY.
 FT DISULFID 189 200 BY SIMILARITY.
 FT DISULFID 250 264 BY SIMILARITY.
 FT DISULFID 367 399 BY SIMILARITY.
 FT DISULFID 377 390 BY SIMILARITY.
 FT DISULFID 424 703 BY SIMILARITY.
 FT DISULFID 444 666 BY SIMILARITY.
 FT DISULFID 476 551 BY SIMILARITY.
 FT DISULFID 500 694 BY SIMILARITY.
 FT DISULFID 510 524 BY SIMILARITY.
 FT DISULFID 521 534 BY SIMILARITY.
 FT DISULFID 592 606 BY SIMILARITY.
 FT DISULFID 644 649 BY SIMILARITY.
 FT METAL 79 79 IRON 1 (BY SIMILARITY).
 FT METAL 111 111 IRON 1 (BY SIMILARITY).
 FT METAL 211 211 IRON 1 (BY SIMILARITY).
 FT METAL 272 272 IRON 1 (BY SIMILARITY).
 FT METAL 414 414 IRON 2 (BY SIMILARITY).
 FT METAL 452 452 IRON 2 (BY SIMILARITY).
 FT METAL 545 545 IRON 2 (BY SIMILARITY).
 FT METAL 614 614 IRON 2 (BY SIMILARITY).
 FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
 FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
 FT BINDING 143 143 SIMILARITY).
 FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
 FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
 FT BINDING 484 484 SIMILARITY).
 FT BINDING 485 485 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
 FT BINDING 485 485 SIMILARITY).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 56 56 I -> V (IN REF. 2).
 FT CONFLICT 88 88 L -> R (IN REF. 2).
 FT CONFLICT 124 124 F -> K (IN REF. 2).
 FT CONFLICT 154 154 F -> P (IN REF. 2).
 FT CONFLICT 304 304 S -> R (IN REF. 2).
 FT CONFLICT 414 414 D -> G (IN REF. 2).
 SQ SEQUENCE 708 AA; 77358 MW; F2ED3C8359960D CRC64;

Query Match 75.7%; Score 53; DB 1; Length 708;
 Best Local Similarity 83.3%; Pred. No. 0.06;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRARVWCAGV 12
 |||||
 Db 359 ARCTRYVWCAGV 370

RESULT 8
 TRFL_MOUSE STANDARD; PRT; 707 AA.

ID TRFL_MOUSE
 AC P08071; P70690; Q61799; Q92292;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T., Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse

RT uterine secretions.";
 RL J. Biol. Chem. 262:10134-10139(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RL Morishi K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.T., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson K.D., Mullaney S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=92042099; PubMed=1939212;
 RA Liu Y., Teng C.T.;
 RT "Characterization of estrogen-responsive mouse lactoferrin promoter.";
 RL J. Biol. Chem. 266:21880-21885(1991).
 CC -1- FUNCTION: TRANSPORTERS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 CC
 DR EMBL, J03298; AAA40525.1; -;
 DR EMBL, D88510; BAA13653.1; -;
 DR EMBL, BC006904; AAH06904.1; -;
 DR EMBL, M74778; AAA39427.1; -;
 DR HSSP, P02788; IC86.
 DR MGD: MGI:96837; LtF.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin. 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN 1; 1.
 DR PROSITE; PS00206; TRANSFERRIN 2; 2.
 DR PROSITE; PS00207; TRANSFERRIN 3; 2.
 KM Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal.
 FT CHAIN 1 19
 FT SIGNAL
 FT CHAIN 20 707
 FT REPEAT 20 357
 FT REPEAT 358 707
 FT DISULFID 27 63
 FT DISULFID 37 54
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 133 216 BY SIMILARITY.
 FT DISULFID 175 191 BY SIMILARITY.
 FT DISULFID 188 199 BY SIMILARITY.
 FT DISULFID 249 263 BY SIMILARITY.
 FT DISULFID 366 398 BY SIMILARITY.
 FT DISULFID 376 389 BY SIMILARITY.
 FT DISULFID 423 702 BY SIMILARITY.
 FT DISULFID 443 665 BY SIMILARITY.
 FT DISULFID 475 550 BY SIMILARITY.
 FT DISULFID 499 693 BY SIMILARITY.
 FT DISULFID 509 523 BY SIMILARITY.
 FT DISULFID 520 533 BY SIMILARITY.
 FT DISULFID 591 605 BY SIMILARITY.
 FT DISULFID 643 648 BY SIMILARITY.
 FT METAL 78 78
 FT METAL 110 110
 FT METAL 210 210
 FT METAL 271 271
 FT METAL 413 413
 FT METAL 451 451
 FT METAL 544 544
 FT METAL 613 613
 FT BINDING 135 135
 FT BINDING 139 139
 FT BINDING 141 141
 FT BINDING 142 142
 FT BINDING 477 477
 FT BINDING 481 481
 FT BINDING 483 483
 FT BINDING 484 484
 FT CARBOHYD 118 118
 FT CARBOHYD 494 494
 FT CONFLICT 1 2
 FT CONFLICT 25 25
 FT CONFLICT 82 82
 FT CONFLICT 359 359
 FT CONFLICT 382 382
 FT CONFLICT 449 449
 FT CONFLICT 629 629
 SQ SEQUENCE 707 AA; 77865 MW; F26AE0340A4C19A8 CRC64;
 Query Match 74.3%; Score 52; DB 1; Length 707;
 Best Local Similarity 75.0%; Pred. No. 0.091;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Cy 1 ARAAPVWCAGV 12
 Db 358 ASKARYWCAGV 369
 RESULT 9
 ICA_PIG STANDARD; FRT; 704 AA.
 AC 029545;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inhibitor of carbonic anhydrase precursor.
 GN ICA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97254619; PubMed=9100029;
 RA Wuebbens M.W., Roush E.D., Decastro C.M., Fierke C.A.;
 RT "Cloning, sequencing, and recombinant expression of the porcine
 inhibitor of carbonic anhydrase: a novel member of the transferrin

RT family.";
 RL Biochemistry 36:4327-4336(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=9309129; PubMed=1463741;
 RA Roush E.D., Fierke C.A.;
 RT "Purification and characterization of a carbonic anhydrase II
 RT inhibitor from porcine plasma.";
 RL Biochemistry 31:12536-12542(1992).
 CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
 CC with nanomolar affinity.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 DR EMBL: U36916; AAB58956.1; -
 DR PIR: I47228; I47228.
 DR HSSP: P19134; 1TFD.
 DR InterPro: IP001136; Transferrin.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KM Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 704 INHIBITOR OF CARBONIC ANHYDRASE.
 FT CARBOHYD 491 491 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 704 AA; 77634 MW; 16B08651931E336 CRC64;
 Query Match 65.7%; Score 46; DB 1; Length 704;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RYVMCAVGE 13
 DB 356 RYVMCAVGE 364
 RESULT 10
 TREE CHICK STANDARD; PRT; 705 AA.
 ID TRFE CHICK
 AC P02789;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovocaptain precursor (Conaluman) (Allergen Gal d 3) (Gal d III)
 DE (Serum transferrin).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8213851; PubMed=7060577;
 RA Jeltsch J.-M., Chambon P.;
 RT "The complete nucleotide sequence of the chicken ovotransferrin
 RT mRNA.";
 RL Eur. J. Biochem. 122:291-295(1982).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=88015626; PubMed=3658709;
 RA Jeltsch J.-M., Hen R., Maroteaux L., Garnier J.-M., Chambon P.;
 RT "Sequence of the chicken ovotransferrin gene.";
 RL Nucleic Acids Res. 15:7643-7645(1987).
 RN [3]
 RP SEQUENCE OF 1-23.
 RC TISSUE=Egg white, and Serum;
 RX MEDLINE=78171533; PubMed=649604;
 RA Thibodeau S.N., Lee D.C., Palmer R.D.;
 RT "Identical precursors for serum transferrin and egg white
 RT conalbumin.";
 RL J. Biol. Chem. 253:3771-3774(1978).
 RN [4]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=82138852; PubMed=6895872;
 RA Williams J., Eilman T.C., Kingston I.B., Wilkins A.G., Kuhn K.A.;
 RT "The primary structure of hen ovotransferrin.";
 RL Eur. J. Biochem. 122:297-303(1982).
 RN [5]
 RP SEQUENCE OF 480-582.
 RX MEDLINE=76039467; PubMed=1172663;
 RA Kingston I.B., Williams J.;
 RT "The amino acid sequence of a carbohydrate-containing fragment of hen
 RT ovotransferrin.";
 RL Biochem. J. 147:463-472(1975).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=70141846; PubMed=4907959;
 RA Eilman T.C., Williams J.;
 RT "The amino acid sequences of cysteine acid-containing peptides from
 RT perlecan acid-oxidized ovotransferrin.";
 RL Biochem. J. 116:515-532(1970).
 RN [7]
 RP REVIEW.
 RX MEDLINE=87190419; PubMed=3032619;
 RA Clifton R.R., Charleaux-Wauters M.;
 RT "Iron transport and storage.";
 RL Eur. J. Biochem. 164:485-506(1987).
 RN [8]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=80068893; PubMed=574451;
 RA Dorland L., Haverkamp J., Vliegenhart J.F., Spik G., Fournet B.,
 RA Montreuil J.;
 RT "Investigation by 360-MHz 1H-nuclear-magnetic-resonance spectroscopy
 RT and methylation analysis of the single glycan chain of chicken
 RT ovotransferrin.";
 RL Eur. J. Biochem. 100:569-574(1979).
 RN [9]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=95186884; PubMed=7881176;
 RA Jacquinet P.M., Leger D., Wieruszski J.M., Coddeville B.,
 RA Montreuil J., Spik G.;
 RT "Change in glycosylation of chicken transferrin glycans biosynthesized
 RT during embryogenesis and primary culture of embryo hepatocytes.";
 RL Glycobiology 4:617-624(1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 24-351.
 RX MEDLINE=94032327; PubMed=8218271;
 RA Dewan J.C., Mikami B., Hirose M., Sacchetti J.C.;
 RT "Structural evidence for a pH-sensitive lysine trigger in the hen
 RT ovotransferrin N-lobe: implications for transferrin iron release.";
 RL Biochemistry 32:11963-11968(1993).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=96083822; PubMed=7490743;
 RA Kurokawa H., Mikami B., Hirose M.;
 RT "Crystal structure of dimeric hen ovotransferrin at 2.4-A
 RT resolution.";
 RL J. Mol. Biol. 254:196-207(1995).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=99428516; PubMed=10497206;
 RA Kurokawa H., Dewan J.C., Mikami B., Sacchetti J.C., Hirose M.;

RT "Crystal structure of hen apo-ovotransferrin. Both lobes adopt an open
 RT conformation upon loss of iron".
 RL J. Biol. Chem. 274:2845-2852(1999).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation to
 CC those of storage and utilization. Serum transferrin may also have
 CC a further role in stimulating cell proliferation.
 CC -1- FUNCTION: TRANSFERRIN HAS A BACTERIOSTATIC FUNCTION. ITS
 CC CONCENTRATION IN AVIAN EGG IS THE HIGHEST CONCENTRATION OF ANY
 CC TRANSFERRIN IN VIVO. TRANSFERRIN IN LIVER IS REGULATED BY THE IRON
 CC LEVELS BUT NOT IN THE OVODUCT. THESE TWO FORMS OF TRANSFERRIN
 CC (LIVER AND OVODUCT) DIFFER ONLY BY THEIR CARBOHYDRATE COMPOSITION.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 DR EMBL: X02009; CA26040.1; -;
 DR EMBL: X00407; CA56468.1; -;
 DR PIR: A26845; TCHE.
 DR PDB: 1NNT; 15-OCT-94.
 DR PDB: 1OVT; 15-SEP-95.
 DR PDB: 1ATV; 29-APR-98.
 DR PDB: 1IE4; 25-DEC-02.
 DR PDB: 1JL4; 19-SEP-01.
 DR PDB: 1NFT; 29-DEC-99.
 DR PDB: 1TFA; 29-DEC-99.
 DR GlycoSuite; P02789; -;
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 KM Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KM Signal; 3D-structure; Allergen; Polymorphism.
 FT SIGNAL 1 19
 FT CHAIN 20 705
 FT REPEAT 20 351
 FT DOMAIN 352 360
 FT REPEAT 361 705
 FT DISULFID 29 64
 FT DISULFID 39 55
 FT DISULFID 134 216
 FT DISULFID 179 193
 FT DISULFID 190 201
 FT DISULFID 247 261
 FT DISULFID 367 399
 FT DISULFID 377 390
 FT DISULFID 424 699
 FT DISULFID 440 662
 FT DISULFID 473 549
 FT DISULFID 497 690
 FT DISULFID 507 521
 FT DISULFID 518 532
 FT DISULFID 589 603
 FT METAL 79 79
 FT METAL 111 111
 FT METAL 210 210
 FT METAL 269 269
 FT METAL 414 414

FT METAL 450 450 IRON 2.
 FT METAL 543 543 IRON 2.
 FT METAL 611 611 IRON 2.
 FT BINDING 136 136 CARBONATE 1.
 FT BINDING 140 140 CARBONATE 1 (VIA AMIDE NITROGEN).
 FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN).
 FT BINDING 143 143 CARBONATE 2.
 FT BINDING 475 475 CARBONATE 2 (VIA AMIDE NITROGEN).
 FT BINDING 479 479 CARBONATE 2 (VIA AMIDE NITROGEN).
 FT BINDING 481 481 CARBONATE 2 (VIA AMIDE NITROGEN).
 FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN).
 FT BINDING 492 492 CARBONATE 2 (VIA AMIDE NITROGEN).
 FT CARBOHYD 83 83 A -> V.
 FT VARIANT 100 100 V -> I.
 FT VARIANT 154 154 R -> W.
 FT VARIANT 239 240 OK -> LN.
 FT VARIANT 686 686 S -> N (IN REF. 1).
 FT CONFLICT 132 132 T -> N (IN REF. 1).
 FT CONFLICT 317 317 L -> F (IN REF. 1).
 FT STRAND 25 30
 FT HELIX 33 46
 FT STRAND 52 57
 FT HELIX 61 69
 FT TURN 70 71
 FT STRAND 75 78
 FT HELIX 80 86
 FT TURN 87 87
 FT TURN 89 91
 FT STRAND 94 100
 FT STRAND 110 118
 FT TURN 119 120
 FT HELIX 125 127
 FT TURN 129 130

Query Match 62.3%; Score 44; DB 1; Length 705;
 Best Local Similarity 58.3%; Pred. No. 2.5;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 RRAVWCAGE 13
 Db 360 RRRIRQCAVCK 371

RESULT 11
 TRFE ANAPL STANDARD; PRT; 686 AA.
 AC P56410;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovotransferrin.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS).
 RA Rawas A., Muirhead H., Williams J.;
 RT "Structure of apo duck ovotransferrin at 2.35-A resolution.";
 RL Acta Crystallogr. D 52:631-640(1996).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS).
 RA Rawas A., Muirhead H., Williams J.;
 RT "Structure of apo duck ovotransferrin: the structures of the N and C
 RT lobes are in the open form."
 RL Acta Crystallogr. D 53:464-468(1997).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation to
 CC those of storage and utilization. Serum transferrin may also have
 CC a further role in stimulating cell proliferation.
 CC -1- FUNCTION: OVOTRANSFERRIN HAS A BACTERIOSTATIC FUNCTION. ITS

Db 341 RENK10MCAVVK 352

```

RESULT 12
REP2_ECOLI
ID REP2_ECOLI STANDARD; PRT; 285 AA.
AC P03066; 047411;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Replication initiation protein.
GN REPA OR REPA1.
OS Escherichia coli.
OC Plasmid IncFII R100, Plasmid IncFII R1, and Plasmid IncFII NR1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII R100;
RX MEDLINE=81074309; PubMed=7003300;
RA Rosen U., Ryder T., Inokuchi H., Ohtsubo H., Ohtsubo E.;
RT "Genes and sites involved in replication and incompatibility of an
RT R100 plasmid derivative based on nucleotide sequence analysis.";
RL Mol. Genet. 179:527-537(1980).
[2]
RP SEQUENCE OF 1-77 FROM N.A.
RC PLASMID=IncFII R100, and IncFII R1;
RX MEDLINE=81173118; PubMed=6163994;
RA Rosen U., Ryder T., Ohtsubo H., Ohtsubo E.;
RT "Role of RNA transcripts in replication incompatibility and copy
RT number control in antibiotic resistance plasmid derivatives.";
RL Nature 290:794-797(1981).
[3]
RP SEQUENCE OF 270-285 FROM N.A.
RC PLASMID=IncFII R1;
RX MEDLINE=88289416; PubMed=3041379;
RA Nasai H., Arai K.;
RT "Repa protein- and oriX-dependent initiation of R1 plasmid
RT replication: identification of a rho-dependent transcription
RT terminator required for cis-action of repA protein.";
RL Nucleic Acids Res. 16:6493-6514(1988).
[4]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII NR1;
RX MEDLINE=89011975; PubMed=3050127;
RA Dong X., Womble D.D., Rownd R.H.;
RT "In-vivo studies on the cis-acting replication initiator protein of
RT IncFII plasmid NR1.";
RL J. Mol. Biol. 202:495-509(1986).
[5]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII NR1;
RX MEDLINE=8510860; PubMed=2580099;
RA Womble D.D., Sampathkumar P., Easton A.M., Luckow V.A., Rownd R.H.;
RT "Transcription of the replication control region of the IncFII
RT R-plasmid NR1 in vitro and in vivo.";
RL J. Mol. Biol. 181:395-410(1985).
[6]
RP SEQUENCE FROM N.A.
RC PLASMID=IncFII R100;
RX MEDLINE=6319522; PubMed=3019092;
RA Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;
RT "DNA replication of the resistance plasmid R100 and its control.";
RL Adv. Biophys. 21:115-133(1986).
CC - FUNCTION: This protein is essential for plasmid replication; it is
CC involved in copy control functions.
CC - SIMILARITY: BELONGS TO THE INCFII REPA FAMILY.
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DR EMBL; J01762; AAA92257.1; -
DR EMBL; J01770; -; NOT ANNOTATED_CDS.
DR EMBL; X12587; CAA31100.1; -
DR EMBL; X12776; CAA31263.1; -
DR EMBL; X02302; CAA26168.1; -
DR EMBL; X02302; CAA26168.1; ALT_INIT.
DR EMBL; M26840; AAA26067.1; -
DR PIR; A03602; IDECRP.
DR PIR; I64780; I64780.
DR InterPro; IPR003446; RepIctn.
DR Pfam; PF02387; IncFII_repa; 1.
KW Plasmid; DNA replication; Plasmid copy control.
FT CONFLICT 55 AA; 32755 MW; A21C9D59D2AB25B CRC64;
SQ SEQUENCE 285 AA; 32755 MW; A21C9D59D2AB25B CRC64;

Query Match 55.7%; Score 39; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARARVW 8
Db 168 ARRSRVW 175

RESULT 13
CSX2_SCHPO
ID CSX2_SCHPO STANDARD; PRT; 870 AA.
AC Q9U9E2; Q09425;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein csx2.
GN CSX2 OR SPBC17G9.08C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OC NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Wolckele G., Aert R., Roben J., Gymnopoulos B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fitz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jhenez J., Moreno S., Armstrong U., Forsburg S.L.,
RA Dominguez A., Revuelta J., Morenno S., Sanchez M., del Rey F., Benito J.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shklovski G.V., Usery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).

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RN [2]
RP SEQUENCE OF 158-345 FROM N.A.
RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
RA Hirata A., Yanagida M.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
CC
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CC
CC EMBL; AL109846; CAB52806.1; -.
CC EMBL; D83419; BAA11920.1; -.
CC PIR; T39731; T39731.
CC
CC GenDB: Spombe: SPBC1799.08c; -.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR001849; HRP-like.
CC InterPro; IPR001849; PH.
CC Pfam; PF01412; ArfGAP; 1.
CC Pfam; PF00169; PH; 1.
CC PRINTS; PR00405; REVINTRACTING.
CC SMART; SM00105; ArfGAP; 1.
CC SMART; SM00233; PH; 1.
CC PROSITE; PS50115; ArfGAP; 1.
CC PROSITE; PS50003; PH_DOMAIN; 1.
CC GTPase activation; Zinc-finger.
CC DOMAIN 510 614 PH.
CC DOMAIN 670 791 ARF-GAP.
CC ZN_FING 686 710 CA-TYPE.
CC CONFLICT 158 166 NGSSPLYLC -> VQVFVLMQ (IN REF. 2).
SQ SEQUENCE 870 AA; 99081 MW; 4B3BD6F6162E80C6 CRC64;

Query Match
Best Local Similarity 54.3%; Score 38; DB 1; Length 870;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ARVWCAV 11
DB 693 ARVWCAI 700

RESULT 14
YH92_AERPE STANDARD; PRT; 176 AA.
AC Q9YB03;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein APE1792.
GN APE1792.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE=93910339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anzai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -1- SIMILARITY: Belongs to the UPF0097 family.

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CC [2]
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CC
CC EMBL; AP00062; BAA80795.1; -.
CC PIR; F72563; F72563.
CC InterPro; IPR004175; 2.5.1_gasee.
CC Pfam; PF02834; 2.5.1_gasee; 2.
CC KX Hypothetical protein; Complete proteome.
SQ SEQUENCE 176 AA; 19666 MW; C8BD5FC929F7E56D CRC64;

Query Match
Best Local Similarity 52.9%; Score 37; DB 1; Length 176;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRVWCAVG 12
DB 72 RRVWVG 81

RESULT 15
TYPE HORSE
ID TYPE HORSE STANDARD; PRT; 706 AA.
AC P27425;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN TF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93277958; PubMed=8504171;
RA Carpenter M.A., Broad T.E.;
RT "The cDNA sequence of horse transferrin.";
RL Biochim. Biophys. Acta 1173:230-232(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Extraembryonic tissue;
RA McDowell K.J., Adams M.H., Baker C.B.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; M69020; AAA30958.1; -.
CC EMBL; U21127; AAA63684.1; -.
CC PIR; S33761; S33761.

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DR HSP; P02787; IABE.
DR InterPro: IPR001156; Transferrin.
DR Pfam: PF00405; transferrin.2.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT CHAIN 20 706 SEROTRANSFERRIN.
FT REPEAT 20 357 1.
FT REPEAT 358 706 2.
FT DISULFID 26 64 BY SIMILARITY.
FT DISULFID 36 55 BY SIMILARITY.
FT DISULFID 134 215 BY SIMILARITY.
FT DISULFID 174 190 BY SIMILARITY.
FT DISULFID 177 198 BY SIMILARITY.
FT DISULFID 187 200 BY SIMILARITY.
FT DISULFID 248 262 BY SIMILARITY.
FT DISULFID 360 623 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 376 389 BY SIMILARITY.
FT DISULFID 423 701 BY SIMILARITY.
FT DISULFID 441 664 BY SIMILARITY.
FT DISULFID 474 550 BY SIMILARITY.
FT DISULFID 498 692 BY SIMILARITY.
FT DISULFID 508 522 BY SIMILARITY.
FT DISULFID 519 533 BY SIMILARITY.
FT DISULFID 590 604 BY SIMILARITY.
FT DISULFID 642 647 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 209 209 IRON 1 (BY SIMILARITY).
FT METAL 270 270 IRON 1 (BY SIMILARITY).
FT METAL 413 413 IRON 2 (BY SIMILARITY).
FT METAL 449 449 IRON 2 (BY SIMILARITY).
FT METAL 544 544 IRON 2 (BY SIMILARITY).
FT METAL 612 612 IRON 2 (BY SIMILARITY).
FT BINDING 136 136 CARBONATE 1 (BY SIMILARITY).
FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 2 (BY SIMILARITY).
FT BINDING 476 476 CARBONATE 2 (BY SIMILARITY).
FT BINDING 480 480 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 483 483 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 706 AA; 78094 MW; 1A0FA566C0409D8A CRC64;
Query Match 52.9%; Score 37; DB 1; Length 706;
Best local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 5 RVTWCavg 12
:|:|:|:|
Db 362 KVMCAIG 369
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Search completed: September 1, 2004, 00:10:42
Job time: 5.58667 secs

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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:56:54 ; Search time 24.0933 Seconds

(without alignments)
170.244 Million cell updates/sec

Title: US-09-508-095-16

Perfect score: 70
Sequence: 1 ARPARVWCAGE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	711	4 Q8TCD2	Q8TCD2 homo sapien
2	70	100.0	711	4 Q8TCH6	Q8TCH6 homo sapien
3	70	100.0	711	4 Q8TCH9	Q8TCH9 homo sapien
4	58	82.9	704	6 Q8WYN8	Q8WYN8 sus scrofa
5	58	82.9	704	6 Q7YS20	Q7YS20 sus scrofa
6	54	77.1	112	6 Q9SM57	Q9SM57 bos taurus
7	54	77.1	355	6 Q8M110	Q8M110 bos taurus
8	52	74.3	707	11 Q8CBA0	Q8CBA0 mus musculu
9	46	65.7	615	5 Q9N9Q6	Q9N9Q6 leishmania
10	45	64.3	383	16 Q88MP5	Q88MP5 pseudomonas
11	45	64.3	383	16 Q886Q4	Q886Q4 pseudomonas
12	45	61.4	383	16 Q914H5	Q914H5 pseudomonas
13	43	61.4	421	11 Q7TP83	Q7TP83 rattus norv
14	43	61.4	700	11 Q9DBD0	Q9DBD0 mus musculu
15	43	61.4	700	11 Q8VC96	Q8VC96 mus musculu
16	42	60.0	783	5 Q8T4D6	Q8T4D6 drosophila

17	42	60.0	1099	10 Q9XFK8	Q9XFK8 zea mays (m
18	42	60.0	1200	10 Q8W5J0	Q8W5J0 oryza sativ
19	42	60.0	1200	10 Q7XD70	Q7XD70 oryza sativ
20	41	58.6	254	16 Q82HU3	Q82HU3 streptomyce
21	41	58.6	279	2 Q8KZS5	Q8KZS5 pseudomonas
22	41	58.6	279	16 Q88RA2	Q88RA2 pseudomonas
23	41	58.6	345	2 Q8KWB8	Q8KWB8 heparitis sp
24	40	57.1	113	12 Q56754	Q56754 bordetella
25	40	57.1	228	16 Q7WGX4	Q7WGX4 bordetella
26	40	57.1	228	16 Q7WGT3	Q7WGT3 bordetella
27	40	57.1	228	16 Q7VYH8	Q7VYH8 bordetella
28	40	57.1	224	4 Q81X02	Q81X02 homo sapien
29	40	57.1	260	16 Q9UR63	Q9UR63 neisseria m
30	40	57.1	339	16 Q8ZQ61	Q8ZQ61 streptomyce
31	40	57.1	342	10 Q82517	Q82517 saccharum h
32	40	57.1	436	16 Q9XA27	Q9XA27 streptomyce
33	40	57.1	483	16 Q9ACW7	Q9ACW7 caulobacter
34	40	57.1	490	10 Q7XTK7	Q7XTK7 zea mays (m
35	40	57.1	509	10 Q41755	Q41755 zea mays (m
36	40	57.1	567	10 Q63342	Q63342 saccharum o
37	40	57.1	567	10 Q63341	Q63341 saccharum r
38	40	57.1	612	13 Q9DDC6	Q9DDC6 melanogramm
39	40	57.1	655	10 Q9LKI9	Q9LKI9 oryza sativ
40	40	57.1	662	10 Q8W430	Q8W430 triticum ae
41	39.5	56.4	129	16 Q9CA30	Q9CA30 mycobacteri
42	39	55.7	291	10 Q9FV5	Q9FV5 arabidopsis
43	39	55.7	294	16 Q88R23	Q88R23 lactobacilli
44	39	55.7	294	16 Q9AAG8	Q9AAG8 caulobacter
45	39	55.7	453	2 Q05147	Q05147 rhodococcus

ALIGNMENTS

RESULT 1
Q8TCD2 PRELIMINARY; PRT; 711 AA.
ID Q8TCD2;
AC Q8TCD2;
BT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Lactotransferrin.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
CC EMBL; BC022347; AA022347.1; -!
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; F:ferric iron binding; IEA.
DR GO; GO:0006826; P:iron ion homeostasis; IEA.
DR GO; GO:0006810; P:iron ion transport; IEA.
DR InterPro; IPR01156; Transferrin.
DR Pfam; PF00405; Transferrin.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMO0094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Iron transport; Metal-binding; Transport.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 100.0%; Score 70; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.00061;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
 |||||
 Db 360 ARARVWCAGE 372

RESULT 2
 Q81Z6 PRELIMINARY; PRT; 711 AA.

AC Q81Z6:
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactoferrin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kaplan J.B., Fine D.H.;
 RT "Characterization of an amino acid polymorphism in the antibacterial
 RT domain of human lactoferrin."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY137470; AAL1304.1; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008199; F:ferric iron binding; IEA.
 DR GO: GO:0006879; P:iron ion homeostasis; IEA.
 DR GO: GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 SO SEQUENCE 711 AA; 78396 MW; 547AB9423C27CE67 CRC64;

Query Match 100.0%; Score 70; DB 4; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
 |||||
 Db 360 ARARVWCAGE 372

RESULT 3
 Q81U92 PRELIMINARY; PRT; 711 AA.

AC Q81U92:
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 LTF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sht Y.-Q., Zhang Y., Zheng Y.-M.;
 RT "Homo sapiens Lactotransferrin Gene: cDNA Cloning and Sequence
 RT Analysis."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 DR GlycoProtein: Iron transport; Metal-binding; Transport.
 FT NON TER 1
 SO SEQUENCE 704 AA; 77681 MW; 64EEF69F7503CC32 CRC64;

Query Match 82.9%; Score 58; DB 6; Length 704;
 Best Local Similarity 83.3%; Pred. No. 0.097;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RT "Homo sapiens lactoferrin (HLF) mRNA.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY165046; AAN6398.1; -;
 DR EMBL: AY178998; AAN75578.2; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008199; F:ferric iron binding; IEA.
 DR GO: GO:0006879; P:iron ion homeostasis; IEA.
 DR GO: GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 DR SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 711
 SO SEQUENCE 711 AA; 78382 MW; 547BFC42C9267E67 CRC64;

Query Match 100.0%; Score 70; DB 4; Length 711;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAGE 13
 |||||
 Db 360 ARARVWCAGE 372

RESULT 4
 Q8WMN8 PRELIMINARY; PRT; 704 AA.

AC Q8WMN8:
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactoferrin (Fragment).
 LTF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang S.-R., Lin T.-Y., Weng C.-N.;
 RT "Isolation and expression of porcine milk lactoferrin."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION. USUALLY BICARBONATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
 DR EMBL: L77887; AAL40161.1; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008199; F:ferric iron binding; IEA.
 DR GO: GO:0006879; P:iron ion homeostasis; IEA.
 DR GO: GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 DR GlycoProtein: Iron transport; Metal-binding; Transport.
 FT NON TER 1
 SO SEQUENCE 704 AA; 77681 MW; 64EEF69F7503CC32 CRC64;

Query Match 82.9%; Score 58; DB 6; Length 704;
 Best Local Similarity 83.3%; Pred. No. 0.097;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 ||:|||||
 355 ARQKVVWCAVG 366

RESULT 5

ID Q7YS20 PRELIMINARY; PRT; 704 AA.
 AC Q7YS20;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactoferrin.
 GN PLF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Pecorini C., Fogher C., Baldi A.;
 RT "The nucleotide sequence of porcine lactoferrin cDNA."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY306198; AAP70487.1; -
 SQ SEQUENCE 704 AA; 77522 MW; AAC8E1767E56BF6A CRC64;

Query Match 82.9%; Score 58; DB 6; Length 704;
 Best Local Similarity 83.3%; Pred. No. 0.097;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 ||:|||||
 DB 355 ARQKVVWCAVG 366

RESULT 6

ID Q9SM57 PRELIMINARY; PRT; 112 AA.
 AC Q9SM57;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-40 FROM N.A.
 RA Li G., Zhang Y., Li N.;
 RT "Analysis of the 5'-region of the bovine lactoferrin gene using PCR-SSCP."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY036583; AAK6816.1; -
 GO GO:0005576; C:extracellular; IEA.
 GO GO:0008199; F:ferriic iron binding; IEA.
 GO GO:0006879; P:iron ion homeostasis; IEA.
 GO GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 FT NON TER 1
 FT NON TER 112
 SQ SEQUENCE 112 AA; 12491 MW; CFE0C1CB3F953FBA CRC64;

Query Match 77.1%; Score 54; DB 6; Length 112;
 Best Local Similarity 83.3%; Pred. No. 0.089;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12

DB 66 ARYTRVWCAVG 77
 ||:|||||

RESULT 7

ID Q8M110 PRELIMINARY; PRT; 355 AA.
 AC Q8M110;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactotransferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 RT "Molecular cloning and sequence analysis of bovine lactotransferrin."
 RL Eur. J. Biochem. 196;177-184 (1991).
 DR EMBL: X17066; CAA34912.1; -
 GO GO:0005576; C:extracellular; IEA.
 GO GO:0008199; F:ferriic iron binding; IEA.
 GO GO:0006879; P:iron ion homeostasis; IEA.
 GO GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; Transferrin; 1.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SMO0094; TR_FER.1.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 355 AA; 38861 MW; 92CFC0274EBC6893 CRC64;

Query Match 77.1%; Score 54; DB 6; Length 355;
 Best Local Similarity 83.3%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARARVWCAVG 12
 ||:|||||
 DB 6 ARYTRVWCAVG 17

RESULT 8

ID Q8CBA0 PRELIMINARY; PRT; 707 AA.
 AC Q8CBA0;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Lactotransferrin.
 GN LTF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RA MEDLINE=22354683; PubMed=12466851;
 RT The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL: AK036491; BAC29450.1; -
 DR MGD: MGI:96837; Ltf.
 GO GO:0005576; C:extracellular; IEA.

DR GO:0008199; F:feric iron binding; IEA.
 DR GO:0006879; P:iron ion homeostasis; IEA.
 DR GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00894; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 SQ SEQUENCE 707 AA; 77837 MW; E1B32F5FD8748A0F CRC64;

Query Match 74.3%; Score 52; DB 11; Length 707;
 Best Local Similarity 75.0%; Pred. No. 1.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 12
 Db 358 ASKARVWCAVG 369

RESULT 9
 Q9N906 PRELIMINARY; PRT; 615 AA.
 AC Q9N906;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN L2464.09.
 OS Leishmania major.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Brown S., Murphy L., Harris D., Ivens A.C., Quail M., Rajandream M.A.,
 RA Barrell B.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RX MEDLINE=98146435; PubMed9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL365154; CAB96741.1;
 DR GO:0005759; Mitochondrial matrix; IEA.
 DR InterPro: IPR003428; MAM33.
 KW Hypothetical protein.
 SQ SEQUENCE 615 AA; 67400 MW; A4AC2CCDB0F2DECB CRC64;

Query Match 65.7%; Score 46; DB 5; Length 615;
 Best Local Similarity 70.0%; Pred. No. 10;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRAVWCA 10
 Db 18 ARSRRLWCA 27

RESULT 10
 Q88MP5 PRELIMINARY; PRT; 383 AA.
 AC Q88MP5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Succinyl-diaminopimelate desuccinylase.
 GN DAPB OR PPI525.
 OS Pseudomonas putida (strain KT2440).
 OC Pseudomonas putida; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423050; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Foute D.B., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., Deboy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chiu Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 RA Uterback T., Rizzo D., Lee K., Kosack D., Moestl D., Medler H.,
 RA Lauber J., Stjepandic D., Hobeisel U., Straetz M., Helm S.,
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL: AE016779; AAN67146.1;
 DR TIGR: PPI525;
 DR GO:0008237; F:metallopeptidase activity; IEA.
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 41238 MW; A75C8A551A95DF36 CRC64;

Query Match 64.3%; Score 45; DB 16; Length 383;
 Best Local Similarity 61.5%; Pred. No. 10;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 13
 Db 158 ARNERLDWCIVGE 170

RESULT 11
 Q886Q4 PRELIMINARY; PRT; 383 AA.
 AC Q886Q4;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Succinyl-diaminopimelate desuccinylase.
 GN DAPB OR PSP01523.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
 RA Berry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,
 RA Dodson R., Deboy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
 RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,
 RA White O., Fraser C., Collier A.;
 RT "Complete sequence of Pseudomonas syringae.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE016861; AA055043.1;
 DR TIGR: PSP01523;
 DR GO:0008237; F:metallopeptidase activity; IEA.
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002933; Peptidase_M20.
 DR Pfam: PF01546; Peptidase_M20; 1.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 41082 MW; B42ABF9558915629 CRC64;

Query Match 64.3%; Score 45; DB 16; Length 383;
 Best Local Similarity 61.5%; Pred. No. 10;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARRAVWCAVG 13

Db 158 ARNERLDMCIVGE 170

RESULT 12

ID Q914H5 PRELIMINARY; PRT; 363 AA.

AC Q914H5; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE Succinyl-diaminopimelate desuccinylase.

GN DAPE OR PA1162

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PAOI;

RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Polger K.R., Kas A., Lapidus K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,

RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an

RT opportunistic pathogen."

RL Nature 406:959-964(2000).

RL EMBL; A5004546; AAG04551.1; -

DR PIR; G83500; G83500.

DR GO; GO:0008237; F-metallopeptidase activity; IEA.

DR GO; GO:0009014; F-succinyl-diaminopimelate desuccinylase acti. .; IEA.

DR GO; GO:0005089; P-lysine biosynthesis via diaminopimelate; IEA.

DR GO; GO:0005089; P-proteolysis and peptidolysis; IEA.

DR InterPro; IPR002933; Peptidase M20.

DR Pfam; PF01546; Peptidase M20; I.

DR TIGRfam; TIGR01246; dape_proteo; 1.

KM Complete proteome.

SQ SEQUENCE 383 AA; 41077 MW; 2283864D40A4272B CRC64;

Query Match 61.4%; Score 43; DB 16; Length 383;

Best Local Similarity 61.5%; Pred. No. 22;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARRARVWCAVGE 13

Db 158 ARGERLDMCIVGE 170

RESULT 13

ID Q7TP83 PRELIMINARY; PRT; 421 AA.

AC Q7TP83; 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE Aa2-001.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Xu C.S., Li W.O., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

RA Yang X.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,

RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;

RT "Liver regeneration after PH."

DR EMBL; AY325160; AAP92561.1; -

SQ SEQUENCE 421 AA; 46104 MW; F7FA0844BD73583A CRC64;

Query Match 61.4%; Score 43; DB 11; Length 421;

Best Local Similarity 77.8%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RVWCAVGE 13

Db 81 RVKCAVQ 89

RESULT 14

ID Q9DBD0 PRELIMINARY; PRT; 700 AA.

AC Q9DBD0; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE 1300017J02Rik protein.

GN 1300017J02Rik.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aikawa T., Hara A., Fukunishi Y., Komoto H., Adachi U., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Scudib F., Suzuki R., Tomita M., Wagner L., Wachi T.,

RA Sakai K., Okido T., Furuno M., Hono H., Baldarelli R., Barch G.,

RA Blake U., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustinchik S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsu S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

DR EMBL; AK005035; BAB23762.1; -

DR HSRF; P19134; ITPD.

DR MGD; MGI:1919025; 1300017J02Rik.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008199; F:ferric iron binding; IEA.

DR GO; GO:0006879; P:iron ion homeostasis; IEA.

DR GO; GO:0006826; P:iron ion transport; IEA.

DR InterPro; IPR001156; Transferrin.

DR Pfam; PF00405; Transferrin_2.

DR PRINTS; PRO0422; TRANSFERRIN.

DR SMART; SMO0094; TR_FER_2.

DR PROSITE; PS00205; TRANSFERRIN_1; 1.

DR PROSITE; PS00207; TRANSFERRIN_3; 1.

SQ SEQUENCE 700 AA; 76765 MW; 38C991D1021AE548 CRC64;

Query Match 61.4%; Score 43; DB 11; Length 700;

Best Local Similarity 77.8%; Pred. No. 39;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RVWCAVGE 13

Db 354 RVKCAVQ 362

RESULT 15

ID Q8VC96 PRELIMINARY; PRT; 700 AA.

Q8VC96

AC Q8VC96;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RIKEN cDNA 1300017J02 gene.
 GN 1300017J02RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021390; AAH21390.1; -;
 DR MGD; MGI:1919025; 1300017J02RIK.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 SQ SEQUENCE 700 AA; 76795 NW; 7DA4A580CB6BF37 CRC64;

Query Match 61.4%; Score 43; DB 11; Length 700;
 Best Local Similarity 77.8%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 RYWCAYGE 13
 |||||:
 Db 354 RYWCAYGQ 362

Search completed: September 1, 2004, 00:15:31
 Job time : 25.0933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:24 ; Search time 132.367 Seconds

(without alignments)
117.402 Million cell updates/sec

Title: US-09-508-095-17

Perfect score: 305

Sequence: 1 YGRRPALAINNPVPRYYA.....YLPNSHPPTVRRPMLHPSF 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29aug04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	305	100.0	55	AAW93881	Bifidobac
2	305	100.0	182	AAW93851	Recombina
3	305	100.0	182	AAW92696	Human kap
4	305	100.0	182	AAW92150	Human mil
5	225.5	73.9	181	AAW18216	Human mol
6	225.5	73.9	181	ADD18210	Human mol
7	71.5	23.4	193	AAW18102	Peptide #
8	71.5	23.4	193	ABW37137	Peptide #
9	71.5	23.4	193	AAW30614	Peptide #
10	71.5	23.4	193	ABW31899	Peptide #
11	71.5	23.4	193	ABW32450	Protein #
12	71.5	23.4	193	AAW02025	Human bon
13	71.5	23.4	193	AAW57857	Human bra
14	71.5	23.4	193	AAW05737	Peptide #
15	71.5	23.4	193	ABW39918	Human pep
16	71.5	23.4	193	ABW31668	Novel hum
17	71.5	23.4	193	ABW31668	Novel hum
18	71.5	23.4	193	ABW31668	Novel hum
19	71.5	23.4	193	ABW31668	Novel hum
20	68.5	22.5	790	ADD85172	Muscul ad
21	68	22.3	334	AAW83194	Sequence
22	67.5	22.1	334	AAW82971	Biocheste
23	67.5	22.1	799	AAW08818	Human pol
24	67.5	22.1	799	ABW70046	Drosophi
25	67.5	22.1	914	AAW24800	Spinoce

26	67.5	22.1	1312	2	AAW33807	Human ata
27	67.5	22.1	1312	2	AAW33495	Human sca
28	67.5	22.1	1312	6	ABW82698	Human sca
29	67.5	22.1	1312	7	ADD18752	Human dis
30	67.5	22.1	1312	2	AAW60213	Spinoce
31	67	22.0	644	6	ABW43313	Canis fam
32	67	22.0	914	4	ABW69998	Drosophi
33	66.5	21.8	273	2	AAW50557	Novel hum
34	66.5	21.8	556	4	ABW05032	Novel hum
35	66	21.6	580	4	AAW60493	Human cel
36	65	21.3	112	3	AAW84457	Amino aci
37	65	21.3	520	7	ADW08749	Novel pro
38	64	21.0	82	4	AAW61243	Propionib
39	64	21.0	82	6	ABW57762	Propionib
40	64	21.0	86	1	AAW83196	Sequence
41	64	21.0	86	1	AAW82973	Biocheste
42	64	21.0	707	4	ABW68526	Drosophi
43	64	21.0	751	2	AAW80839	Japanese
44	64	21.0	899	4	ABW25235	Novel hum
45	64	21.0	1729	4	ABW62538	Drosophi

ALIGNMENTS

RESULT 1	AAW93881	standard; peptide; 55 AA.
AC	XX	AAW93881;
DT	XX	27-AUG-2003 (revised)
DT	XX	25-JUN-1999 (first entry)
DE	XX	Bifidobacterium bifidus stimulating peptide 17.
KW	XX	Bifidogenic peptide; protease; treatment; microbe-related disease;
KW	XX	bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
KW	XX	infection; inflammation; microbial induced tumour; degenerative disorder;
KW	XX	diarrhoea; colic; oral microflora; intestinal microflora; caries;
KW	XX	vaginal microflora.
OS	XX	Bifidobacterium bifidum.
PN	XX	WO9914231-A2.
PD	XX	25-MAR-1999.
PF	XX	16-SEP-1998; 98WO-EP005899.
PR	XX	16-SEP-1997; 97DE-01040604.
PR	XX	11-FEB-1998; 98DE-01005385.
PI	XX	(FORS/ FORSSMAN W.
PI	XX	Forsmann W, Zucht H, Liepke C;
DR	XX	WPI, 1999-244022/20.
PT	XX	Milk-derived peptides that stimulate Bifidobacterium bifidus.
PS	XX	Claim 2, Page 3, 25pp; German.
CC	XX	This invention describes milk-derived bifidogenic peptides and their
CC	XX	active derivatives or fragments, and combinations of them produced by
CC	XX	chemical coupling. Such are produced from bovine or human milk by
CC	XX	treatment for 2 hr with proteases, then centrifuging to remove fat and
CC	XX	acidifying to pH 2 to precipitate proteins. The solution phase is then
CC	XX	subjected to reverse-phase high-performance liquid chromatography (HPLC)
CC	XX	and cation-exchange HPLC, the fractions adjusted to salt content below 25
CC	XX	mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
CC	XX	Bifidobacterium bifidus and Escherichia coli in presence of the
CC	XX	fractions. Those fractions for which (BW-B0) -(BW-E0) is at least 0.15 are

CC selected where Bw = germ count after 16 hr culture of *B. bifidus* in 50%
CC Rikher broth containing peptide at 0.2 mg/ml, B0 = germ count under
CC similar conditions in a peptide-free control. Bw = germ count after 16 hr
CC culture of *E. coli* in 3 g/l tryptic broth containing peptide at 0.2
CC mg/ml, B0 = germ count under similar conditions in a peptide-free
CC control. The peptides AAW93865-W9388 are used to treat microbe-related
CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
CC oral, intestinal or vaginal microflora, or carries. (Updated on 27-AUG-
CC 2003 to correct OS field.)

XX
SQ Sequence 55 AA;

Query Match 100.0%; Score 305; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.9e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 55
DB 1 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 55

RESULT 2
AAR939351

ID AAR939351 standard; protein; 182 AA.

XX
AC AAR939351;

XX 25-MAR-2003 (revised)
DT 26-JAN-1994 (first entry)

XX Recombinant human kappa casein.

XX Casein; supplement; milk; pharmaceutical; ss.

XX Homo sapiens.

XX MO9315196-A1.

XX 05-AUG-1993.

XX 25-JAN-1993; 93WO-DK000024.

XX 23-JAN-1992; 92DK-00000088.

XX (SYMB-) SYMBICOM AB.

XX Hansson L, Stroemqvist M, Bergstroem S, Hernell O, Toernell J;

XX WPI; 1993-258675/32.

XX N-PSDB; AAQ46850.

XX DNA encoding human kappa-casein - used for obtaining recombinant
PT polypeptide(s) for use as nutrient supplements, partic. in infant
PT formulae.

XX Claim 44; Page 88-89; 110pp; English.

CC The recombinant human kappa casein is produced in high yields by means of
CC either a eukaryotic or prokaryotic expression system. It is used as a
CC nutrient supplement in milk based products to provide a substantial
CC improvement of the nutritional and biological value of the formulae,
CC making it closer in similarity to human milk. It can also be used as a
CC pharmaceutical. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 182 AA;

Query Match 100.0%; Score 305; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 55

DB 63 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 117

RESULT 3

ID AAR72696 standard; protein; 182 AA.

XX AAR72696;

XX 06-NOV-1995 (first entry)

XX Human kappa-casein.

XX Kappa-casein; milk protein.

XX Homo sapiens.

XX US5391497-A.

XX 21-FEB-1995.

XX 13-OCT-1992; 92US-00962569.

XX 13-OCT-1992; 92US-00962569.

XX (COLS) UNIV COLORADO FOUND INC.

XX Ham RG, Jeffers KF, Menon RS, Chang Y;

XX WPI; 1995-160470/21.

XX N-PSDB; AAQ83598.

XX DNA encoding human kappa-casein - used for the prodn. of large amts. of
PT highly purified kappa-casein milk protein for infant use.

XX Disclosure; Col 13-16; 14pp; English.

XX A commercial cDNA library prepd. in lambda gtl1 from mRNA obtd. from
CC human breast tissue removed during the third trimester of pregnancy was
CC screened with rabbit anti-bovine kappa-casein cDNA. The cDNA insert of a
CC recombinant phage was amplified by PCR to obtain a full-length clone
CC (AAQ89598) encoding human kappa-casein (AAR72696)

XX
SQ Sequence 182 AA;

Query Match 100.0%; Score 305; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 55
DB 63 YORRPAIAINNPVPTTYANPAVVRPAAQIPQROYLPNSHPPTVVRPNLHPSF 117

RESULT 4

ID AAR92150 standard; protein; 182 AA.

XX AAR92150;

XX 24-OCT-1996 (first entry)

XX Human milk kappa-casein, inhibits rotaviral infection.

XX Milk protein; kappa-casein; rotavirus inhibition; gastroenteritis;
KW infant formulation; immunodeficiency; diarrhoea.

XX Homo sapiens.

XX WO9608269-A1.

PD 21-MAR-1996.

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XX PF 05-MAY-1995; 95WO-US005676.
XX XX
XX PR 16-SEP-1994; 94US-00308882.
XX PR 16-SEP-1994; 94US-00308883.
XX PA (ABBO ) ABBOTT LAB.
XX PI Mukerji P, Prieto PA, Seo AE, Saxter JH, Cummings RD;
XX DR WPI; 1996-179724/18.
XX PT Kappa-casein used as anti-rotaviral infection agent in nutritional
XX PT product - to prevent, retard or treat rotavirus infection, especially in
XX PT infants, children and immuno-deficient patients.
XX PS Claim 1; Fig 9; 42pp; English.
XX CC AAP2150 is human milk kappa-casein which is useful as a component of an
XX CC enteral nutritional product. Kappa-casein has anti-rotaviral activity, it
XX CC inhibits the attachment of human rotavirus to mammalian cells. The kappa-
XX CC casein is useful in the treatment and prevention of onset of
XX CC gastroenteritis and other diarrhoeal diseases caused by rotaviridae esp.
XX CC in infants, children or immunodeficient patients. Kappa-casein appeared
XX CC to have no side effects on the subjects treated and is unlikely to be
XX CC toxic or cause an allergic reaction
XX SQ Sequence 182 AA;

Query Match 100.0%; Score 305; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQRRPAIAINNPVRYTYANPAVVRPAHQIQPQRYLPSNSHPTVVRPNLHPSF 55
DB 63 YQRRPAIAINNPVRYTYANPAVVRPAHQIQPQRYLPSNSHPTVVRPNLHPSF 117

RESULT 5
AAE18216
ID AAE18216 standard; protein; 181 AA.
AC AAE18216;
XX XX
DT 07-MAY-2002 (first entry)
DE Human MOL6 protein.
XX XX
XX KW Secretd molecule; MOL6 protein; MOLX; cardiomyopathy; atherosclerosis;
XX KW diabetes; chromosomal disorder; albinism; anaemia; psoriasis; scarring;
XX KW liver cirrhosis; neurodegeneration; osteoarthritis; organ rejection;
XX KW cerebral thrombosis; hypertension; systemic lupus erythematosus; asthma;
XX KW immune disease; ischaemia; immunodeficiency; rheumatoid arthritis; ulcer;
XX KW HIV; human immuno deficiency virus; hepatitis; haemostatic disease; pain;
XX KW haemotopoietic; thrombolytic; thrombocytopaenia; Alzheimer's disease;
XX KW Parkinson's disease; Huntington's disease; muscular disease; stress;
XX KW ocular disease; growth disorder; depression; epilepsy; contraceptive;
XX KW vulnerrary; osteopahic; haemostatic; tranquiliser; antidepressant;
XX KW analgesic; vasotropic; hypotensive; gene therapy.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FH 1.24
XX FT /label= Signal_peptide
XX FT 25.181
XX FT Protein /label= Mature_MOL6_protein
XX XX
XX PN MO200206339-A2.
XX XX
XX PD 24-JAN-2002.
XX XX
XX PF 03-JUL-2001; 2001WO-US021249.

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XX XX
XX PR 03-JUL-2000; 2000US-0215854P.
XX PR 03-JUL-2000; 2000US-0215856P.
XX PR 03-JUL-2000; 2000US-0215902P.
XX PR 07-JUL-2000; 2000US-0216585P.
XX PR 07-JUL-2000; 2000US-0216586P.
XX PR 07-JUL-2000; 2000US-0216722P.
XX PR 17-JUL-2000; 2000US-0218632P.
XX PR 17-JUL-2000; 2000US-0218982P.
XX PR 27-JUL-2000; 2000US-0221285P.
XX PR 14-FEB-2001; 2001US-0268734P.
XX PR 08-MAR-2001; 2001US-0274260P.
XX PR 29-MAR-2001; 2001US-0279856P.
XX PA (CURA-) CURAGEN CORP.
XX XX
XX PI Spaderna SK, Tchernev V, Liu X, Shenoy S, Spytek K, Zernhusen B;
XX PI Paturajan M, Taupier RJ, Rastelli L, Grose WM, Szekeres ES;
XX PI Alabrook J, Lopley DW, Shen L, Burgess CE, Shinkets RA, Padigaru M;
XX XX
XX DR WPI; 2002-155038/20.
XX DR N-PSDB; AAD28950.
XX XX
XX PT Nucleic acids encoding secreted polypeptides, designated MOLX
XX PT polypeptides, useful for treating a MOLX-associated disorder, e.g.
XX PT cardiomyopathy, atherosclerosis, diabetes and metabolic disorders.
XX PS Claim 1; Page 78; 223pp; English.
XX XX
XX CC The patent discloses nucleic acid sequences encoding novel secreted
XX CC molecule (MOL) polypeptides, designated MOLX polypeptides (i.e. a MOL
XX CC protein where X is an integer from 1 to 8). Sequences of the invention
XX CC are useful for treating or preventing a MOLX-associated disorder in
XX CC humans. They are useful for treating or preventing cardiomyopathy,
XX CC atherosclerosis and disorders related to cell signal processing and
XX CC metabolic pathway modulation. The MOLX antibodies are useful for treating
XX CC or preventing diabetes and disorders related to cell signal processing
XX CC and metabolic pathway modulation. MOLX sequences are useful for the
XX CC treatment or diagnosis of other MOLX-associated disorders, e.g.
XX CC chromosomal disorders, albinism, anaemia, liver cirrhosis, psoriasis,
XX CC scarring, neurodegeneration, osteoarthritis, organ rejection, cerebral
XX CC thrombosis, ischaemia, hypertension, systemic lupus erythematosus, immune
XX CC diseases, immunodeficiency, HIV (human immuno deficiency virus), viral,
XX CC bacterial and fungal infections, hepatitis, rheumatoid arthritis, asthma,
XX CC haematopoietic, thrombolytic, haemostatic diseases, thrombocytopaenia,
XX CC ulcers, Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX CC ocular disease, muscular diseases, growth disorders, loss of libido,
XX CC stress, depression, pain and epilepsy. They are useful for preventing
XX CC chemotherapy side effects and as contraceptives. Sequences of the
XX CC invention are also useful for gene therapy. The present sequence is human
XX CC kappa casein precursor-like protein, MOL6
XX SQ Sequence 181 AA;

Query Match 73.9%; Score 225.5; DB 5; Length 181;
Best Local Similarity 81.8%; Pred. No. 1.6e-19;
Matches 45; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 YQRRPAIAINNPVRYTYANPAVVRPAHQIQPQRYLPSNSHPTVVRPNLHPSF 55
DB 63 YQRRPAIAINNPVRYTYANPAVVRPAHQIQPQRYLPSNSHPTVVRPNLHPSF 116

RESULT 6
ADD18210
ID ADD18210 standard; protein; 181 AA.
AC ADD18210;
XX XX
XX DT 15-JAN-2004 (first entry)
XX DE Human molecule (MOL) protein MOL6.
XX XX

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KM molecule protein; MOL protein; MOLX agonist; MOLX antagonist;
 KM cardiant; antidiabetic; antiarteriosclerotic; gene therapy;
 KM MOLX-associated disorder; cardiomyopathy; diabetes; atherosclerosis;
 KM human; MOle.

XX Homo sapiens.

XX WO2003003984-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021268.

XX 05-JUL-2001; 2001US-0303168P.

XX 05-JUL-2001; 2001US-0303241P.

XX 26-SEP-2001; 2001US-00965212.

XX 26-SEP-2001; 2001US-00965545.

XX 01-APR-2002; 2002US-0368986P.

XX 01-APR-2002; 2002US-0369065P.

XX 08-MAY-2002; 2002US-0378730P.

XX 30-MAY-2002; 2002US-0384327P.

XX 07-JUN-2002; 2002US-0386816P.

XX 17-JUN-2002; 2002US-00174372.

XX (CURA-) CITRAGEN CORP.

XX Fernandes ER, Vernet CAM, Shimkets RA, Anderson DW, Padigam M;
 PI Boldog FL, Li L, Shenoy SG, Casman SJ, Rastelli L, Alsobrook JP;
 PI Burgess CE, Grosse WM, Gusev VY, Ujw, Lepley DM, Liu X, Mezick AJ;
 PI Patilrajani M, Shen L, Spaderna SK, Spytek KA, Szekeres ES;
 PI Taupier RJ, Tchernev VT, Zernusen BD, Voss EZ;

XX WPI; 2003-210304/20.

XX N-PSDB; ADD18209.

XX New MOLX polypeptide; nucleic acid or MOLX-specific antibody, useful for
 PT preparing a composition for treating or preventing a MOLX-associated
 PT disorder, e.g., cardiomyopathy, diabetes or atherosclerosis.

XX Claim 1; SEQ ID NO 20; 371pp; English.

XX This invention relates to novel human nucleic acid sequences which encode
 CC novel molecule (MOL) proteins numbered MOL1-23, referred to generally in
 CC the specification as MOLX. Compounds which modulate the function of the
 CC MOLX proteins of the invention, MOLX agonists or antagonists, may have
 CC cardiant, antidiabetic or antiarteriosclerotic activities. In addition,
 CC the DNA and protein sequences disclosed may prove useful for gene
 CC therapy. The protein, nucleic acid or antibody is useful for preparing a
 CC composition for treating or preventing a MOLX-associated disorder, for
 CC example cardiomyopathy, diabetes or atherosclerosis. The present sequence
 CC is the amino acid sequence of a MOL protein of the invention.

XX Sequence 181 AA;

XX Query Match 73.9%; Score 225.5; DB 7; Length 181;
 Best Local Similarity 81.8%; Pred. No. 1.6e-19;
 Matches 45; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

XX 1 YGRFPALINNYVPRITYANPAVVRP-NAQIPQRYLPSHPPTVRRPNNLHP 55
 Db 63 YGRFPALINNYVPRITYANPAVVRP-NAQIPQRYLPSHPPTVRRPNNLHP 116

XX RESULT 7

XX AAM18102

XX AAM18102 standard; protein; 193 AA.

XX AAM18102;

XX 12-OCT-2001 (first entry)

XX Peptide #4536 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;
 KM cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 22928; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes
 CC (SENPs; see A110068-A1128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 193 AA;

XX Query Match 23.4%; Score 71.5; DB 4; Length 193;
 Best Local Similarity 36.0%; Pred. No. 1.1; 23; Indels 5; Gaps 2;
 Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;

XX 5 PAIAINNPYVPRITYANPAVVRP-NAQIPQRYLPSHPPTVRRPNNLHP 53
 Db 15 PAIAINNPYVPRITYANPAVVRP-NAQIPQRYLPSHPPTVRRPNNLHP 60

XX RESULT 8

XX ABB37137

XX ABB37137 standard; peptide; 193 AA.

XX ABB37137;

XX 04-FEB-2002 (first entry)

XX Peptide #4643 encoded by human foetal liver single exon probe.

XX Human, foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human fetal liver.
 XX
 PS Claim 27; SEQ ID NO 29772; 639pp + Sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human fetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 193 AA;
 XX
 Query Match 23.4%; Score 71.5; DB 4; Length 193;
 Best Local Similarity 36.0%; Pred. No. 1.1; Indels 5; Gaps 2;
 Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;
 QY 5 PAIAINNPVPRTYANPAVVRP-HAQIPORQYLPNSHPPTVVRPNLHP 53
 Db 15 PAPAHHP-----EYQGQPVVSHPHIMPQGHVAPPPPPPPISHMPHP 60
 XX
 RESULT 9
 ID AAM30614 standard; protein; 193 AA.
 XX
 AC AAM30614;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #4651 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 XX genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-48897/53.

XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 27; SEQ ID NO 30883; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see A131315-A157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 193 AA;
 XX
 Query Match 23.4%; Score 71.5; DB 4; Length 193;
 Best Local Similarity 36.0%; Pred. No. 1.1; Indels 5; Gaps 2;
 Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;
 QY 5 PAIAINNPVPRTYANPAVVRP-HAQIPORQYLPNSHPPTVVRPNLHP 53
 Db 15 PAPAHHP-----EYQGQPVVSHPHIMPQGHVAPPPPPPPISHMPHP 60
 XX
 RESULT 10
 ID ABB31899 standard; peptide; 193 AA.
 XX
 AC ABB31899;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Peptide #4550 encoded by breast cell single exon nucleic acid probe.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 XX cancer.
 XX
 OS Homo sapiens.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX
 PS Claim 27; SEQ ID NO 14867; 327pp + Sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or

prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 193 AA;

Query Match 23.4%; Score 71.5; DB 4; Length 193;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;

QY 5 PAIAINNPVPRTYANPAVVRP-HAQIPORQYLPNSHPPTVVRPNLHP 53
DB 15 PAPAHHHP-----EYQGQPVVSHPHHIMPQOHYAPPPPPPPISHMPHP 60

RESULT 11
ABB22450
ID ABB22450 standard; protein; 193 AA.
AC ABB22450;

DT 23-JAN-2002 (first entry)

DE Protein #4449 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;
KW Cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

OS Homo sapiens.

PN W0200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR,

WPI; 2001-488899/53.

PT Single exon nucleic acid probes for analyzing gene expression in human hearts.

PS Claim 15; SEQ ID NO 24220; 530pp; English.

The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABB21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting of the diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed

specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 193 AA;

Query Match 23.4%; Score 71.5; DB 4; Length 193;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;

QY 5 PAIAINNPVPRTYANPAVVRP-HAQIPORQYLPNSHPPTVVRPNLHP 53
DB 15 PAPAHHHP-----EYQGQPVVSHPHHIMPQOHYAPPPPPPPISHMPHP 60

RESULT 12
AAM70275
ID AAM70275 standard; protein; 193 AA.
AC AAM70275;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30581.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukemia; lymphoma; myeloma.

OS Homo sapiens.

PN W0200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

PS Example 4; SEQ ID NO 30581; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention

Sequence 193 AA;

Query Match 23.4%; Score 71.5; DB 4; Length 193;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;

QY 5 PAIAINNPVPRTYANPAVVRP-HAQIPORQYLPNSHPPTVVRPNLHP 53
DB 15 PAPAHHHP-----EYQGQPVVSHPHHIMPQOHYAPPPPPPPISHMPHP 60

RESULT 13

AAM57857
ID AAM57857 standard; protein; 193 AA.
XX
AC AAM57857;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29962.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
PS Example 4; SEQ ID NO 29962; 650bp + Sequence Listing; English.
XX
SQ The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 193 AA;
XX
Query Match 23.4%; Score 71.5; DB 4; Length 193;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;
OY 5 PAIAINPVPRITYANPAVVR-HAQIPQRCYLPNSHPTVRRBNLHP 53
DB 15 PAPAHHNP---EYQGQPVVSHPHHIMPQCHYAPPPPPPPPSHMP 60
RESULT 14
ID AAM05737 standard; protein; 193 AA.
XX
AC AAM05737;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #4419 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
OS Homo sapiens.
XX

PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
PS Claim 27; SEQ ID NO 14477; 322bp; English.
XX
SQ The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AI110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridizes at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer; disorders of development,
CC inflammatory diseases of the breast; fibrocystic changes; proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 193 AA;
XX
Query Match 23.4%; Score 71.5; DB 4; Length 193;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 18; Conservative 4; Mismatches 23; Indels 5; Gaps 2;
OY 5 PAIAINPVPRITYANPAVVR-HAQIPQRCYLPNSHPTVRRBNLHP 53
DB 15 PAPAHHNP---EYQGQPVVSHPHHIMPQCHYAPPPPPPPPSHMP 60
RESULT 15
ID ABG39918 standard; peptide; 193 AA.
XX
AC ABG39918;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29583.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karsagen syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
OS Homo sapiens.
XX
PN WO200186003-A2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:04:10 : Search time 35.5667 Seconds

(Without alignments)
79.834 Million cell updates/sec

Title: US-09-508-095-17

Perfect score: 305

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Scoring table:

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

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6: /cgn2_6/prodata/2/iaa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	182	1	US-07-962-569A-8
2	305	100.0	182	1	US-08-308-883-2
3	305	100.0	182	1	US-08-730-163-2
4	305	100.0	182	3	US-08-256-799-2
5	305	100.0	182	3	US-08-462-437-2
6	288	97.7	182	3	US-08-462-437-31
7	68	22.3	331	6	5202236-37
8	68	22.3	334	6	5202236-3
9	67.5	22.1	1312	3	US-09-041-886-19
10	67.5	22.1	1312	4	US-09-648-281-2
11	67.5	22.1	1312	4	US-09-707-919A-19
12	67.5	22.1	1312	4	US-09-083-268-3
13	66	21.6	297	4	US-09-252-991A-18170
14	65.5	21.5	822	4	US-09-252-991A-21920
15	64	21.0	86	6	5202236-7
16	64	21.0	691	4	US-09-252-991A-16809
17	63	20.7	202	6	5202236-36
18	63	20.7	203	6	5202236-1
19	63	20.7	652	6	5202236-13
20	63	20.7	744	6	5202236-25
21	62.5	20.5	417	4	US-09-252-991A-22460
22	62.5	20.5	628	4	US-09-252-991A-18780
23	61.5	20.2	161	4	US-09-252-991A-30695
24	61	20.0	865	4	US-09-281-766-19
25	60.5	19.8	144	4	US-09-252-991A-21500
26	60.5	19.8	292	4	US-09-252-991A-22366
27	60.5	19.8	636	4	US-09-252-991A-24902

28	59.5	19.5	298	4	US-09-252-991A-31845	Sequence 31845, A
29	59.5	19.5	726	4	US-09-252-991A-20675	Sequence 20675, A
30	59	19.3	394	4	US-09-252-991A-19344	Sequence 19344, A
31	59	19.3	476	4	US-09-252-991A-27078	Sequence 27078, A
32	58.5	19.2	462	4	US-09-976-594-427	Sequence 427, App
33	58.5	19.2	697	4	US-09-252-991A-25363	Sequence 25363, A
34	58	19.0	634	4	US-09-614-912-88	Sequence 88, Appl
35	58	19.0	634	4	US-09-614-912-100	Sequence 100, App
36	58	19.0	663	4	US-09-252-991A-30843	Sequence 30843, A
37	58	19.0	1009	4	US-09-252-991A-24492	Sequence 24492, A
38	57.5	18.9	281	1	US-07-800-364B-14	Sequence 14, Appl
39	57.5	18.9	281	3	US-07-989-847-12	Sequence 12, Appl
40	57.5	18.9	281	3	US-08-468-411-12	Sequence 12, Appl
41	57.5	18.9	281	4	US-09-780-601A-12	Sequence 12, Appl
42	57.5	18.9	315	4	US-09-252-991A-16743	Sequence 16743, A
43	57.5	18.9	399	5	PCT-US91-07635-6	Sequence 6, Appl
44	57.5	18.9	402	1	US-07-841-646-29	Sequence 29, Appl
45	57.5	18.9	402	1	US-07-901-703-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-07-962-569A-8
; Sequence 8, Application US/07962569A
; Patent No. 5391497
;
GENERAL INFORMATION:
;
APPLICANT: MENON, RAVI S.
;
APPLICANT: JEFFERS, KATHLEEN F.
;
APPLICANT: CHANG, YING-FON
;
APPLICANT: HAM, RICHARD G.
;
TITLE OF INVENTION: HUWAN K-CASEIN
;
NUMBER OF SEQUENCES: 8
;
CORRESPONDENCE ADDRESS:
;
ADDRESSER: FREDERICK W. PEPPER, PH.D.
;
STREET: 11545 W. BERNARDO COURT, STE. 302
;
CITY: SAN DIEGO
;
STATE: CA
;
COUNTRY: USA
;
ZIP: 92127
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: Patentin Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/07/962,569A
;
FILING DATE: 19921013
;
CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
;
NAME: PEPPER PH.D., FREDERICK W.
;
REGISTRATION NUMBER: 31,286
;
REFERENCE/DOCKET NUMBER: 920224.01
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (619) 451-1120
;
TELEFAX: (619) 451-9628
;
INFORMATION FOR SEQ ID NO: 8:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 182 amino acids
;
TYPE: AMINO ACID
;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
US-07-962-569A-8
;
Query Match 100.0%; Score 305; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 YORPPAIAINNPVPRYYAIPORQYLPNSHPVTRRPNLHPSF 55
Db 63 YORPPAIAINNPVPRYYAIPORQYLPNSHPVTRRPNLHPSF 117
```

RESULT 2
US-08-308-883-2
Sequence 2, Application US/08308883
Patent No. 5576300
GENERAL INFORMATION:
APPLICANT: Mukerji, P.
APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E.-Y.
APPLICANT: Baxter, J. H.
APPLICANT: Cummings, R. D.
TITLE OF INVENTION: Method for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: Ross Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: United States
ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,883
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 5576300 applicable
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFAX: (614) 624-3074
TELEX: No. 5576300e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: Amino acid
STRANDEDNESS:
MOLECULE TYPE: Linear
DESCRIPTION:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein,
JOURNAL: Process for Obtaining the Protein and Use The

VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER: PCT/WO93/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
US-08-308-883-2
Query Match 100.0%; Score 305; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 YORPAAIANNPVPRYYANPAVVRPAQIPQRYLPNSHPPTVVRPNLHPSF 55
Db 63 YORPAAIANNPVPRYYANPAVVRPAQIPQRYLPNSHPPTVVRPNLHPSF 117
RESULT 3
US-08-730-163-2
Sequence 2, Application US/08730163
Patent No. 5712250
GENERAL INFORMATION:
APPLICANT: Mukerji, P.
APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E.-Y.
APPLICANT: Baxter, J. H.
APPLICANT: Cummings, R. D.
TITLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: Ross Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: United States
ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B)COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1(D)SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,882
FILING DATE: 16-SEP-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFAX: (614) 624-3074
TELEX: No. 5712250e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: Amino acid
STRANDEDNESS:
MOLECULE TYPE: Linear
DESCRIPTION:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:

CELL LINE:
ORGANISM: HUMAN
IMMEDIATE SOURCE: HUMAN
LIBRARY: HUMAN
CLONE: HUMAN
POSITION IN GENOME: HUMAN
CHROMOSOME/SEGMENT: HUMAN
MAP POSITION: HUMAN
UNITS: HUMAN
FEATURE: HUMAN
NAME/KEY: HUMAN
LOCATION: HUMAN
IDENTIFICATION METHOD: HUMAN
OTHER INFORMATION: HUMAN
PUBLICATION INFORMATION: HUMAN
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL: HUMAN
VOLUME: HUMAN
ISSUE: HUMAN
PAGES: HUMAN
DATE: HUMAN
DOCUMENT NUMBER: PCT/WO93/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO: HUMAN
US-08-730-163-2

Query Match 100.0%; Score 305; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 55
DB 63 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 117

RESULT 4
US-08-256-799-2
Sequence 2, Application US/08256799
Patent No. 6222094
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROMQVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELI, Oile
APPLICANT: TOERNELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-799-2

Query Match 100.0%; Score 305; DB 3; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 55
DB 63 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 117

RESULT 5
US-08-462-437-2
Sequence 2, Application US/08462437
Patent No. 6232094
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROMQVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELI, Oile
APPLICANT: TOERNELL, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-437-2

Query Match 100.0%; Score 305; DB 3; Length 182;
Best Local Similarity 100.0%; Pred. No. 5.3e-30;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 55
DB 63 YORPPALAINNPVPRITYANPAVVRPHAQIPQROYLPNSHPPTVRRRNLPSPF 117

Db 63 YORRPAIAINNPVPRITYANPAVVRPHAQIPORQYLPNSHPTVVRPNLHPSF 117

RESULT 6
US-08-462-437-31
Sequence 31, Application US/08462437

Patent No. 6232094

GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: STROEMOVIK, Mats

APPLICANT: BERGSTROM, Sven

APPLICANT: HERRELL, Olie

APPLICANT: TOERNELL, Jan

TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS

TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,437

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 86/92

FILING DATE: 23-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: HANSSON-1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 182 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-462-437-31

Query Match 97.7%; Score 298; DB 3; Length 182;
Best Local Similarity 98.2%; Pred. No. 3.8e-29;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 YORRPAIAINNPVPRITYANPAVVRPHAQIPORQYLPNSHPTVVRPNLHPSF 55
Db 63 YORRPAIAINNPVPRITYANPAVVRPHAQIPORQYLPNSHPTVVRPNLHPSF 117

RESULT 7
5202236-37
Patent No. 5202236

APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,

SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE

PROTEIN

NUMBER OF SEQUENCES: 39

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/528,762

FILING DATE: 25-MAY-1990

APPLICATION NUMBER: 82,456

FILING DATE: 07-AUG-1987

APPLICATION NUMBER: 933,945

FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
SEQ ID NO: 37
LENGTH: 331
5202236-37

Query Match 22.3%; Score 68; DB 6; Length 331;
Best Local Similarity 29.3%; Pred. No. 1.1;
Matches 17; Conservative 9; Mismatches 28; Indels 4; Gaps 2;

Y 1 YORRPAIAINNPVPRITYA--NPVVRPHAQIPORQYLPNSHPTVVRPNLHPSF 55
Db 127 YKAKPTYKI-KPTVPSTYKAKPTNPSTYKAKPSYPTTYKAKSPPTTYKAKSPPTTY 183

RESULT 8
5202236-37

Patent No. 5202236

APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,

SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE

PROTEIN

NUMBER OF SEQUENCES: 39

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/528,762

FILING DATE: 25-MAY-1990

APPLICATION NUMBER: 82,456

FILING DATE: 07-AUG-1987

APPLICATION NUMBER: 933,945

FILING DATE: 24-NOV-1986

APPLICATION NUMBER: 650,128

FILING DATE: 13-SEP-1984

SEQ ID NO: 37

LENGTH: 334

5202236-37

Query Match 22.3%; Score 68; DB 6; Length 334;
Best Local Similarity 29.3%; Pred. No. 1.1;
Matches 17; Conservative 9; Mismatches 28; Indels 4; Gaps 2;

Y 1 YORRPAIAINNPVPRITYA--NPVVRPHAQIPORQYLPNSHPTVVRPNLHPSF 55
Db 130 YKAKPTYKI-KPTVPSTYKAKPTNPSTYKAKPSYPTTYKAKSPPTTYKAKSPPTTY 186

RESULT 9
US-09-041-886-19
Sequence 19, Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:

APPLICANT: Bredesen, Dale E.

APPLICANT: Rabizadeh, Sharoz

TITLE OF INVENTION: Proapoptotic Peptides, Dependence

TITLE OF INVENTION: Polypeptides and Methods of Use

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,886

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-19

Query Match 22.1%; Score 67.5; DB 4; Length 1312;
Best Local Similarity 40.0%; Pred. No. 6.4;
Matches 16; Conservative 3; Mismatches 18; Indels 3; Gaps 1;

QY 15 PRTYANPAVVRPHAIPOROYLPNSHPPTVVRPNLHPS 54
DB 563 PSRYOGSPNSLPRAATPTR---PPSRPPSRPSRPSHPS 599

RESULT 10
US-09-648-281-2
Sequence 2, Application US/09648281
Patent No. 6515197
GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M.
TITLE OF INVENTION: Transgenic Animal Model of
FILE REFERENCE: P-CE 4336
CURRENT APPLICATION NUMBER: US/09/648,281
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1312
TYPE: PRT
ORGANISM: Homo sapien
US-09-648-281-2

Query Match 22.1%; Score 67.5; DB 4; Length 1312;
Best Local Similarity 40.0%; Pred. No. 6.4;
Matches 16; Conservative 3; Mismatches 18; Indels 3; Gaps 1;

QY 15 PRTYANPAVVRPHAIPOROYLPNSHPPTVVRPNLHPS 54
DB 563 PSRYOGSPNSLPRAATPTR---PPSRPPSRPSRPSHPS 599

RESULT 11
US-09-707-919A-19
Sequence 19, Application US/09707919A
Patent No. 6623927
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: Method for detection of human sphocerebeller ataxia 2
FILE REFERENCE: US 443
CURRENT APPLICATION NUMBER: US/09/707,919A
CURRENT FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 1312
TYPE: PRT
ORGANISM: Homo sapiens
US-09-707-919A-19

Query Match 22.1%; Score 67.5; DB 4; Length 1312;
Best Local Similarity 40.0%; Pred. No. 6.4;
Matches 16; Conservative 3; Mismatches 18; Indels 3; Gaps 1;

QY 15 PRTYANPAVVRPHAIPOROYLPNSHPPTVVRPNLHPS 54
DB 563 PSRYOGSPNSLPRAATPTR---PPSRPPSRPSRPSHPS 599

RESULT 12
US-09-083-268-3
Sequence 3, Application US/09083268
Patent No. 6673535
GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M.
TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Mueller, Raasch & Gebhardt, P.A.
STREET: 119 No. 6673535th Fourth Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/727,084
FILING DATE: 08-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 232.00010101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-268-3

Query Match 22.1%; Score 67.5; DB 4; Length 1312;
Best Local Similarity 40.0%; Pred. No. 6.4;
Matches 16; Conservative 3; Mismatches 18; Indels 3; Gaps 1;

QY 15 PRTYANPAVVRPHAIPOROYLPNSHPPTVVRPNLHPS 54
DB 563 PSRYOGSPNSLPRAATPTR---PPSRPPSRPSRPSHPS 599

RESULT 13
US-09-252-991A-18170
Sequence 18170, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:15:50 ; Search time 125.4 Seconds
(without alignments)
137,988 Million cell updates/sec

Title: US-09-508-095-17

Perfect score: 305

Sequence: 1 YGRRPALAINPYVRYTYA.....YLPNGHPVVRPLHPSF 55

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 31461289 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	182	15	US-10-190-115-50
2	305	100.0	182	15	US-10-190-115-52
3	305	100.0	182	15	US-10-190-115-53
4	305	100.0	182	15	US-10-369-072-50
5	305	100.0	182	15	US-10-369-072-52
6	305	100.0	182	15	US-10-369-072-53
7	298	97.7	182	15	US-10-190-115-51
8	298	97.7	182	15	US-10-369-072-51
9	230	75.4	181	15	US-10-190-115-99
10	230	75.4	181	15	US-10-369-072-99
11	225.5	73.9	181	15	US-10-190-115-20
12	225.5	73.9	181	15	US-10-369-072-20
13	165	54.1	182	15	US-10-190-115-54
14	165	54.1	182	15	US-10-369-072-54
15	76.5	25.1	184	12	US-10-424-599-265601

16	76.5	25.1	413	13	US-10-062-254-270	Sequence 270, App
17	71.5	23.4	193	9	US-09-864-761-37748	Sequence 37748, A
18	71.5	23.4	440	12	US-10-087-192-1168	Sequence 1168, Ap
19	71.5	23.4	486	12	US-10-087-192-1165	Sequence 1185, Ap
20	70	23.0	405	12	US-10-092-900A-268	Sequence 268, App
21	69	22.6	328	12	US-10-424-599-238959	Sequence 238959, App
22	69	22.6	828	15	US-10-369-493-3414	Sequence 3414, Ap
23	67.5	22.1	777	12	US-10-424-599-222602	Sequence 222602, App
24	67.5	22.1	1312	14	US-10-141-541-6	Sequence 6, Appl1
25	67	22.0	644	14	US-10-259-451-2	Sequence 2, Appl1
26	66.5	21.8	569	16	US-10-437-963-142298	Sequence 142298, A
27	66	21.6	303	12	US-10-425-114-47692	Sequence 47692, A
28	66	21.6	384	12	US-10-424-599-238957	Sequence 238957, A
29	65.5	21.5	151	16	US-10-437-963-140070	Sequence 140070, A
30	65.5	21.5	185	16	US-10-437-963-181433	Sequence 181433, A
31	65.5	21.5	425	13	US-10-425-114-67068	Sequence 67068, A
32	65	21.3	425	13	US-10-062-254-274	Sequence 274, App
33	65	21.3	428	12	US-10-425-114-52415	Sequence 52415, A
34	64.5	21.1	735	15	US-10-369-493-2328	Sequence 2328, Ap
35	64	21.0	278	12	US-10-425-114-71179	Sequence 71179, A
36	64	21.0	427	12	US-10-425-114-45447	Sequence 45447, A
37	64	21.0	534	12	US-10-425-114-39261	Sequence 39261, A
38	64	21.0	542	12	US-10-424-599-244216	Sequence 244216, A
39	64	21.0	545	12	US-10-425-114-38986	Sequence 38986, A
40	64	21.0	546	12	US-10-425-114-39265	Sequence 39265, A
41	63.5	20.8	351	13	US-10-029-217A-7	Sequence 7, Appl1
42	63.5	20.8	424	12	US-10-424-599-248498	Sequence 248498, A
43	63.5	20.8	486	16	US-10-437-963-181048	Sequence 181048, A
44	63	20.7	81	14	US-10-083-357-1283	Sequence 1283, Ap
45	63	20.7	202	12	US-10-425-114-47897	Sequence 47897, A

ALIGNMENTS

RESULT 1
US-10-190-115-50
; Sequence 50, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosche, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigara, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shumkecs, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernyev, Vajizhar T.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/366,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 50
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-190-115-50

Query Match 100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQRRPAIANNPVPTTYANPAVVRPHAQIPQROYLPNSHPTVVRRLHPSF 55
Db 63 YQRRPAIANNPVPTTYANPAVVRPHAQIPQROYLPNSHPTVVRRLHPSF 117

RESULT 2
US-10-190-115-52
Sequence 52, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT: Alschbrook, John P. II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosse, William M.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Lepley, Denise M.
APPLICANT: Liu, Xiaohong
APPLICANT: Mezick, Amanda J.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Shen, Lei
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Szekeres, Edward S. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Zehrusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME.
FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856

PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585,
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 52
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-190-115-52

Query Match 100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQRRPAIANNPVPTTYANPAVVRPHAQIPQROYLPNSHPTVVRRLHPSF 55
Db 63 YQRRPAIANNPVPTTYANPAVVRPHAQIPQROYLPNSHPTVVRRLHPSF 117

RESULT 3
US-10-190-115-53
Sequence 53, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT: Alschbrook, John P. II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosse, William M.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Lepley, Denise M.
APPLICANT: Liu, Xiaohong
APPLICANT: Mezick, Amanda J.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Shen, Lei
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Szekeres, Edward S. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Zehrusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03


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PRIORITY APPLICATION NUMBER: 60/216,585,
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuroSeqList version 0.1
SEQ ID NO 53
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (19)..(19)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (20)..(20)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (21)..(21)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (22)..(22)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (23)..(23)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (24)..(24)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (25)..(25)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (26)..(26)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (27)..(27)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (28)..(28)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc.feature
LOCATION: (29)..(29)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-10-190-115-53

```

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Query Match      100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YORRPAIAINNPVPRITYYANPAVVRPHAQIPQROYLPSNSHPTVVRPNLHPSF 55
DB 63 YORRPAIAINNPVPRITYYANPAVVRPHAQIPQROYLPSNSHPTVVRPNLHPSF 117

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RESULT 4
US-10-369-072-50
Sequence 50, Application US/10369072

```

```

Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Paturajan, Meera
APPLICANT: Taupier, Raymond T
APPLICANT: Rastelli, Luca
APPLICANT: Grose, William M
APPLICANT: Szerkes, Edward S
APPLICANT: Lepley, Denise M
APPLICANT: Shen, Lei
APPLICANT: Burgess, Catherine E
APPLICANT: Shinkets, Richard
APPLICANT: Padigaru, Muralidhara
TITLE OR INVENTION: No. US20040014081A1 proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT FILING DATE: US/10/369,072
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/898,994
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-072-50

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Query Match      100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YORRPAIAINNPVPRITYYANPAVVRPHAQIPQROYLPSNSHPTVVRPNLHPSF 55
DB 63 YORRPAIAINNPVPRITYYANPAVVRPHAQIPQROYLPSNSHPTVVRPNLHPSF 117

```

```

RESULT 5
US-10-369-072-52
Sequence 52, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan

```

```

; APPLICANT: Paturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grose, William M
; APPLICANT: Szerkes, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-369-072-52

Query Match      100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1,5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 55
Db 63 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 117

RESULT 6
US-10-369-072-53
; Sequence 53, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grose, William M
; APPLICANT: Szerkes, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (19)..(29)
; OTHER INFORMATION: wherein Xaa is any amino acid/
; US-10-369-072-53

Query Match      100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1,5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 55
Db 63 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 117

RESULT 7
US-10-190-115-51
; Sequence 51, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Grose, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szerkes, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
```

```

; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (19)..(29)
; OTHER INFORMATION: wherein Xaa is any amino acid/
; US-10-369-072-53

Query Match      100.0%; Score 305; DB 15; Length 182;
Best Local Similarity 100.0%; Pred. No. 1,5e-26;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 55
Db 63 YORRPALNNPVPRTYYANPAVVRPHAQIPQROYLPNSHPPTVVRRLNHPSF 117

RESULT 7
US-10-190-115-51
; Sequence 51, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Grose, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szerkes, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
```

```
/ APPLICANT: Zethusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585,
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2001-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 51
/ LENGTH: 182
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-190-115-51

Query Match          97.7%; Score 298; DB 15; Length 182;
Best Local Similarity 98.2%; Pred. No.9.3e-26;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQRRPAAIANNPYPRITYANPAVVRPAAQIPQRYLPNSHPPTVVRPNLHPSF 55
DB 63 YQRRPAAIANNPYPRITYANPAVVRPAAQIPQRYLPNSHPPTVVRPNLHPSF 117

RESULT 8
US-10-369-072-51
/ Sequence 51, Application US/10369072
/ Publication No. US20040014081A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Spaderna, Stephen K
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zethusen, Bryan
/ APPLICANT: Patnirajan, Meera
/ APPLICANT: Taupier, Raymond T
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Grosse, William M
/ APPLICANT: Szekeres, Edward S
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Shen, Lei
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Padigaru, Muralidhara
/ TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-050 CON2
/ CURRENT APPLICATION NUMBER: US/10/369,072
/ CURRENT FILING DATE: 2003-02-18
/ PRIOR APPLICATION NUMBER: 10/174,372
/ PRIOR FILING DATE: 2002-06-17
/ PRIOR APPLICATION NUMBER: 09/898,994
```

```
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 60/218,992
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 51
/ LENGTH: 182
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-369-072-51

Query Match          97.7%; Score 298; DB 15; Length 182;
Best Local Similarity 98.2%; Pred. No.9.3e-26;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQRRPAAIANNPYPRITYANPAVVRPAAQIPQRYLPNSHPPTVVRPNLHPSF 55
DB 63 YQRRPAAIANNPYPRITYANPAVVRPAAQIPQRYLPNSHPPTVVRPNLHPSF 117

RESULT 9
US-10-190-115-99
/ Sequence 99, Application US/10190115
/ Publication No. US20030207394A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook, John P. II
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Grosse, William M.
/ APPLICANT: Gusev, Vladimyr Y.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Mezick, Amanda J.
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Patnirajan, Meera
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Shen, Lei
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shimkets, Steven K.
/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zethusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
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PRIOR APPLICATION NUMBER: 60/215,854
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,856
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,902
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/216,585,
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,586
 PRIOR FILING DATE: 2001-07-07
 PRIOR APPLICATION NUMBER: 60/216,722
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/218,622
 PRIOR FILING DATE: 2000-07-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 136
 SOFTWARE: CuraSeqList version 0.1
 SEQ ID NO 99
 LENGTH: 181
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-190-115-99

Query Match 75.4%; Score 230; DB 15; Length 181;
 Best Local Similarity 74.5%; Pred. No. 4,1e-18;
 Matches 41; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

CY 1 YORRPATNNPVPRTYVNPAYVRPHAOIPORQYLPNSHPTVYRRNLHPSF 55
 DB 63 YORRPATNNPVPRTYVNPAYVRPHAOIPORQYLPNSHPTVYRRNLHPSF 117

RESULT 10
 US-10-369-072-99
 Sequence 99, Application US/10369072
 Publication No. US20040014081A1
 GENERAL INFORMATION:
 APPLICANT: Alsobrook II, John P
 APPLICANT: Spaderma, Stephen K
 APPLICANT: Tchernev, Vellizar
 APPLICANT: Liu, Xiaohong
 APPLICANT: Shenoy, Suresh
 APPLICANT: Spytek, Kimberly
 APPLICANT: Zethusen, Bryan
 APPLICANT: Patturajan, Meera
 APPLICANT: Taupier, Raymond T
 APPLICANT: Rastelli, Luca
 APPLICANT: Groses, William M
 APPLICANT: Szekeres, Edward S
 APPLICANT: Lepley, Denise M
 APPLICANT: Shen, Lei
 APPLICANT: Burgess, Catherine E
 APPLICANT: Shimkets, Richard
 APPLICANT: Padigaru, Muralidhara
 TITLE OF INVENTION: No. US0090014081A1el Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-050 CON2
 CURRENT APPLICATION NUMBER: US/10369,072
 CURRENT FILING DATE: 2003-02-18
 PRIOR APPLICATION NUMBER: 10/174,372
 PRIOR FILING DATE: 2002-06-17
 PRIOR APPLICATION NUMBER: 09/898,994
 PRIOR FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: 60/215,854
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,856
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,902
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/216,585
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,586
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,722

PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/218,622
 PRIOR FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 60/218,992
 PRIOR FILING DATE: 2000-07-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 99
 LENGTH: 181
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Domain search
 US-10-369-072-99

Query Match 75.4%; Score 230; DB 15; Length 181;
 Best Local Similarity 74.5%; Pred. No. 4,1e-18;
 Matches 41; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

CY 1 YORRPATNNPVPRTYVNPAYVRPHAOIPORQYLPNSHPTVYRRNLHPSF 55
 DB 63 YORRPATNNPVPRTYVNPAYVRPHAOIPORQYLPNSHPTVYRRNLHPSF 117

RESULT 11
 US-10-190-115-20
 Sequence 20, Application US/10190115
 Publication No. US20030207394A1
 GENERAL INFORMATION:
 APPLICANT: Alsobrook, John P. II
 APPLICANT: Boldog, Ferenc L.
 APPLICANT: Burgess, Catherine E.
 APPLICANT: Casman, Stacie J.
 APPLICANT: Groses, William M.
 APPLICANT: Gusev, Vladimir Y.
 APPLICANT: U, Weizhen
 APPLICANT: Lepley, Denise M.
 APPLICANT: Liu, Xiaohong
 APPLICANT: Mezik, Amanda J.
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Patturajan, Meera
 APPLICANT: Rastelli, Luca
 APPLICANT: Shen, Lei
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Spaderma, Steven K.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Taupier, Raymond T.
 APPLICANT: Tchernev, Vellizar T.
 APPLICANT: Zethusen, Bryan D.
 APPLICANT: Voss, Edward Z.
 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-050 CIP
 CURRENT APPLICATION NUMBER: US/10/190,115
 CURRENT FILING DATE: 2003-02-10
 PRIOR APPLICATION NUMBER: 60/303,168
 PRIOR FILING DATE: 2001-07-05
 PRIOR APPLICATION NUMBER: 60/368,996
 PRIOR FILING DATE: 2002-04-01
 PRIOR APPLICATION NUMBER: 60/386,816
 PRIOR FILING DATE: 2002-06-07
 PRIOR APPLICATION NUMBER: 60/215,854
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,856
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,902
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/216,585,
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,586

;; PRIOR FILING DATE: 2001-07-07
;; PRIOR APPLICATION NUMBER: 60/216,722
;; PRIOR FILING DATE: 2000-07-07
;; PRIOR APPLICATION NUMBER: 60/218,622
;; PRIOR FILING DATE: 2000-07-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 136
;; SOFTWARE: Curaseqdist version 0.1
;; SEQ ID NO 20
;; LENGTH: 181
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-190-115-20

Query Match 73.9%; Score 225.5; DB 15; Length 181;
Best Local Similarity 81.8%; Pred. No. 1.3e-17;
Matches 45; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 YQRRPAIAINNPYRTYYANPAVVRPRAQIPQRCYLPNSHPPTVVRRLHPSPF 55
Db 63 YKRRPAIALNNQYGLRTYYATQAVVRAHAQIPQRCYLPNSH-HTVVRRLHPSPF 116

RESULT 12
US-10-369-072-20
; Sequence 20, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchenev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grose, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/998,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20

;; LENGTH: 181
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-369-072-20

Query Match 73.9%; Score 225.5; DB 15; Length 181;
Best Local Similarity 81.8%; Pred. No. 1.3e-17;
Matches 45; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 YQRRPAIAINNPYRTYYANPAVVRPRAQIPQRCYLPNSHPPTVVRRLHPSPF 55
Db 63 YKRRPAIALNNQYGLRTYYATQAVVRAHAQIPQRCYLPNSH-HTVVRRLHPSPF 116

RESULT 13
US-10-190-115-54
; Sequence 54, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grose, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchenev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/368,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Curaseqdist version 0.1
; SEQ ID NO 54
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-190-115-54

Query Match 54.1%; Score 165; DB 15; Length 182;
Best Local Similarity 58.2%; Pred. No. 8,6e-11;
Matches 32; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 YGRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTVRRPNLHPSF 55
DB 63 YGRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTVRRPNLHPSF 117

RESULT 14

US-10-369-072-54
; Sequence 54, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grose, William M
; APPLICANT: Szerkes, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-072-54

Query Match 54.1%; Score 165; DB 15; Length 182;
Best Local Similarity 58.2%; Pred. No. 8,6e-11;
Matches 32; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 YGRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTVRRPNLHPSF 55
DB 63 YGRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTVRRPNLHPSF 117

RESULT 15

US-10-424-599-265601
; Sequence 265601, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 265601
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(164)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81858C.1.pep
US-10-424-599-265601

Query Match 25.1%; Score 76.5; DB 12; Length 164;
Best Local Similarity 38.6%; Pred. No. 0.7;
Matches 17; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 2 QRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTV 45
DB 22 QRRPAIANNPVPRITYANPAVVRPHQIIPQROYLNSHPPTV 62

Search completed: September 1, 2004, 00:49:21
Job time: 127.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:03:45; Search time 31.9 Seconds

(without alignments)
165.847 Million cell updates/sec

Title: US-09-508-095-17

Sequence: 1 YGRAPAIANNPYPRTYA.....YLPNSHPVWRPNLHPSF 55

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r78:*
2: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	305	100.0	182	1	KKHU	casein kappa precu
2	160	52.5	188	2	A48382	kappa-casein - pig
3	129	42.3	171	1	KKGT	kappa-casein - goa
4	129	42.3	192	2	S15513	kappa-casein - goa
5	127	41.6	190	1	KKRB	kappa-casein precu
6	124	40.7	192	1	KKRA	kappa-casein precu
7	119	39.0	180	2	UC4955	kappa-casein precu
8	93	30.5	234	2	S12092	kappa-casein precu
9	73.5	24.1	352	2	T06482	probable cell wall
10	69.5	22.8	340	1	MMBE11	latency-related pr
11	68	22.3	381	2	S53985	cell wall protein
12	65	21.3	389	2	AB2667	hypothetical prote
13	65	21.3	875	2	S23760	polysaccharid adhes
14	65	21.3	1400	2	T52359	hypothetical prote
15	64.5	21.1	254	2	T25073	hypothetical prote
16	64.5	21.1	735	2	T40619	hypothetical prote
17	64	21.0	751	2	S68957	neutral trehalase
18	62	20.3	173	2	A72450	adhesive plaque pr
19	62	20.3	346	2	S19129	hypothetical prote
20	61.5	20.2	607	2	AH2891	proline-rich prote
21	61.5	20.2	644	2	D97667	thiamin biosynthes
22	61	20.0	516	2	H71332	hypothetical prote
23	61	20.0	628	2	S19150	hypothetical prote
24	60.5	19.8	238	2	T40820	proline-rich prote
25	60.5	19.8	329	2	T10064	cytokinin-induced
26	60.5	19.8	506	2	C81704	monooxygenase-rela
27	60.5	19.8	753	2	UQ0332	Op protein - Kenna
28	60	19.7	306	2	T52340	cell wall-plasma m
29	60	19.7	636	2	T03439	probable ethylene-

30	60	19.7	2297	2	T34918	polyketide synthas
31	59.5	19.5	307	2	S10015	alpha/beta-gliadin
32	59.5	19.5	663	2	T40493	hnt-3/forhead tra
33	59.5	19.5	848	4	A44282	retrovirus-related
34	59.5	19.5	977	2	T16232	hypothetical prote
35	59.5	19.5	982	2	T06576	hypothetical prote
36	59	19.3	838	2	T04449	probable protein k
37	58.5	19.2	301	2	UQ1663	hypothetical prote
38	58.5	19.2	335	2	B9591	hybrid proline-ric
39	58.5	19.2	335	2	T52078	proline-rich prote
40	58.5	19.0	1285	2	T14171	proline-rich prote
41	58	19.0	256	2	C64228	ataxin-2 - mouse
42	58	19.0	366	2	S37864	hypothetical prote
43	58	19.0	459	2	S51302	probable transcrip
44	58	19.0	830	2	A60369	S103 protein-bind
45	57.5	18.9	164	2	T15525	nitrate reductase
						hypothetical prote

ALIGNMENTS

RESULT 1

KKHU
casein kappa precursor [validated] - human
N:Alternate names: kappa-casein
N:Contains: caseinoglycopeptide
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence-revision 03-Oct-1995 #text-change 08-Dec-2000
C:Accession: UC4957; A56638; A24001; A16604; S22070
R:Edlund, A.; Johansson, T.; Leidvik, B.; Hansson, L.
Gene 174, 65-69, 1996
A>Title: Structure of the human kappa-casein gene.
A:Reference number: UC4957; MUID:97017129; PMID:8863730
A:Accession: UC4957
A:Molecule type: DNA
A:Residues: 1-182 <EDL>
A:Cross-references: GB:U51899; NID:G1245481; PIDN:AAC50772.1; PID:G1245482
R:Bergetrom, S.; Hansson, L.; Hennell, O.; Loennekedal, B.; Nilsson, A.K.; Stroemqvist, DNA Seq. 3, 245-246, 1992
A>Title: Cloning and sequencing of human kappa-casein cDNA.
A:Reference number: A56638; MUID:93208373; PMID:1256818
A:Accession: A56638
A:Molecule type: mRNA
A:Residues: 1-182 <BER>
A:Cross-references: EMBL:X66417; NID:G29675; PIDN:CAA47048.1; PID:G29676
A:Experimental source: lactating mammary gland (NCBI:P:128264)
R:Brignon, G.; Choufrou, A.; Ribadeau-Dumas, B.
FEBS Lett. 188, 48-54, 1985
A>Title: Preparation and amino acid sequence of human kappa-casein.
A:Reference number: A24001; MUID:85258132; PMID:4018271
A:Accession: A24001
A:Molecule type: protein
A:Residues: 1-25-26-28-123 <BRI>
A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have R,F,faa, A.M.; Jolles, J.; Aubert, J.P.; Louchoux-Lefebvre, M.H.; Jolles, P.
Eur. J. Biochem. 111, 333-339, 1980
A>Title: Localisation and importance of the sugar part of human casein.
A:Reference number: A16604; MUID:811144; PMID:7460900
A:Accession: A16604
A:Molecule type: protein
A:Residues: 118-160, TT', 163-172, 'P', 174-177, 'PTS', 182 <FIA>
C:Comment: This protein is only a minor component in human milk, whereas it is a cows ml C:Genetics:
A:Gene: GDB:CSN10; cask; CSN3; Kca
A:Cross-references: GDB:5916337; OMIM:601695
A:Map position: 4q21.1-4q21.1
A:Introns: 18/3; 29/3
A>Note: the first intron occurs before the initiator codon
C:Superfamily: kappa-casein
C:Keywords: glycoprotein; mammary gland; milk; pyroglutamic acid
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-182/Product: kappa-casein #status experimental <VAT>

F:118-182/Product: caseinoglycopeptide #status experimental <CGP>
 F:23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
 F:117-118/Cleavage site: Phe-Tle (cysteine) #status experimental
 F:133,143,151,157,167,169,178,181/Binding site: carboxylate (Thr) (covalent) #status
 F:162/Binding site: carboxylate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 305; DB 1; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.8e-27;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQRRPAIANNPYVPTTYANPAVVRPHAIQIPQRYLPSNHPPTVRRPNLHPSF 55
 DB 63 YQRRPAIANNPYVPTTYANPAVVRPHAIQIPQRYLPSNHPPTVRRPNLHPSF 117

RESULT 2

A48382
 kappa-casein - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 19-Nov-1993 #sequence _revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A48382; A12717
 R:Levine, W.B.; Alexander, L.J.; Hoganson, G.E.; Beattie, C.W.
 Ann. Genet. 23, 361-363, 1992
 A:Title: Cloning and sequencing of the porcine kappa-casein cDNA.
 A:Reference number: A48382; MUID:92367959; PMID:1503275
 A:Accession: A48382
 A:Status: preliminary
 A:Residues: 1-188 <REV>
 A:Molecule type: nucleic acid
 A:Cross-references: GB:X51977; GB:SA2402; NID:9406774; PIDN:CAA3623.1; PID:9406775
 A:Experimental source: mammary gland backbone (NCBIN:110878, NCBI:110880)
 A:Note: sequence extracted from NCBI backbone
 R:Chobert, J.M.; Mercier, J.C.; Baby, C.; Haze, G.
 FEBS Lett. 72, 173-178, 1976
 A:Title: Structure primaire du caseinomacropéptide des caseines kappa porcine et humaine
 A:Reference number: A12717; MUID:77068846; PMID:1001463
 A:Accession: A12717
 A:Molecule type: protein
 A:Residues: 118-188 <CHO>
 C:Superfamily: kappa-casein

Query Match 52.5%; Score 160; DB 2; Length 188;
 Best Local Similarity 54.5%; Pred. No. 6.4e-11;
 Matches 30; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 YQRRPAIANNPYVPTTYANPAVVRPHAIQIPQRYLPSNHPPTVRRPNLHPSF 55
 DB 63 YQRRSAVSPNRCFIPYVYARPVVAGPHAKQKQWCDQPVVPTVARRRPHASF 117

RESULT 3

KKGB
 kappa-casein - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 24-Apr-1984 #sequence _revision 24-Apr-1984 #text_change 31-Dec-2000
 C:Accession: A94479; A90670; A03114
 R:Mercier, J.C.; Addo, F.; Pelissier, J.P.
 unpublished results, cited by Mercier, J.C., Chobert, J.M., and Addo, F., FEBS Lett. 72
 A:Description: Comparative study of the amino acid sequences of the caseinomacropéptides
 A:Reference number: A94479
 A:Accession: A94479
 A:Molecule type: protein
 A:Residues: 1-171 <EBL>
 A:Note: the amino-terminal residue appears to be pyrrolidone carboxylic acid, but cycliz
 R:Mercier, J.C.; Addo, F.; Pelissier, J.P.
 Biochimie 58, 1303-1310, 1976
 A:Title: Structure primaire du caseinomacropéptide de la caseine K caprine.
 A:Reference number: A90670; MUID:77112689; PMID:1016651
 A:Accession: A90670
 A:Molecule type: protein
 A:Residues: 106-171 <ME2>
 A:Note: 119-Val was also found
 A:Note: Ser-151 and Ser-168 are phosphorylated

C:Comment: Chymosin hydrolyzes the peptide bond between Phe-105 and Met-106.
 C:Superfamily: kappa-casein
 C:Keywords: mammary gland; milk; phosphoprotein

Query Match 42.3%; Score 129; DB 1; Length 171;
 Best Local Similarity 44.4%; Pred. No. 1.8e-07;
 Matches 28; Conservative 6; Mismatches 21; Indels 8; Gaps 1;

QY 1 YQRRPAIANNPYVPTTYANPAVVRPHAIQIPQRYLPSNHPPTVRRPNLHPSF 52
 DB 43 YQRRPAIANNQFLPPYVAKPVAVRSPAQTLQWQLPVTVPKAKSCQDQPTTLARPHPH 102

QY 53 PSF 55
 DB 103 LSF 105

RESULT 4

S15513
 kappa-casein - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence _revision 20-Feb-1995 #text_change 13-Aug-1999
 C:Accession: S15513
 R:Coll, A.; Folch, J.M.; Sanchez, A.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S15513
 A:Accession: S15513
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-192 <COL>
 A:Cross-references: EMBL:X60763; NID:9977; PIDN:CAA43174.1; PID:9978
 C:Superfamily: kappa-casein
 C:Keywords: phosphoprotein

Query Match 42.3%; Score 129; DB 2; Length 192;
 Best Local Similarity 44.4%; Pred. No. 2e-07;
 Matches 28; Conservative 6; Mismatches 21; Indels 8; Gaps 1;

QY 1 YQRRPAIANNPYVPTTYANPAVVRPHAIQIPQRYLPSNHPPTVRRPNLHPSF 52
 DB 64 YQRRPAIANNQFLPPYVAKPVAVRSPAQTLQWQLPVTVPKAKSCQDQPTTLARPHPH 123

QY 53 PSF 55
 DB 124 LSF 126

RESULT 5

KKBOB
 kappa-casein precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence _revision 23-Mar-1995 #text_change 16-Jun-2000
 C:Accession: S02076; B23071; S06376; JN0364; A91206; A90033; A90920; A91634; A90592; A60
 R:Alexander, L.J.; Stewart, A.F.; Mackinlay, A.G.; Kapelinskaya, T.V.; Tkach, T.M.; Goro
 Eur. J. Biochem. 178, 395-401, 1988
 A:Title: Isolation and characterization of the bovine kappa-casein gene.
 A:Reference number: S02076; MUID:59091174; PMID:3208764
 A:Contents: A variant
 A:Accession: S02076
 A:Molecule type: DNA
 A:Residues: 1-190 <ALB>
 A:Cross-references: EMBL:X14907; NID:9177; PIDN:CAA33034.1; PID:91228078
 R:Stewart, A.F.; Willis, I.M.; Mackinlay, A.G.
 Nucleic Acids Res. 12, 3895-3907, 1984
 A:Title: Nucleotide sequences of bovine alpha-s1- and kappa-casein cDNAs.
 A:Reference number: A93517; MUID:84221403; PMID:6328443
 A:Contents: A variant
 A:Accession: B23071
 A:Molecule type: mRNA
 A:Residues: 1-190 <STE>
 A:Cross-references: GB:X00565; NID:9170; PIDN:CAA5231.1; PID:91364187
 R:Gorodetski, S.I.; Kaledin, A.S.
 Sov. Genet. 23, 398-404, 1987

A>Title: Analysis of nucleotide sequence of bovine kappa-casein cDNA.
 A/Reference number: S06376
 A/Contents: B2 variant
 A/Accession: S06376
 A/Molecule type: mRNA
 A/Residues: 1-138, 'G', 140-156, 'I', 158-168, 'A', 170-173, 'T', 175-190 <GOR>
 R/Gorodetskiy, S.I.; Kershulite, D.D.; Korobko, B.G.
 Bioorg. Khim. 9, 1693-1694, 1983
 A>Title: Primary structure of cDNA of Bos taurus kappa-casein macropепptide.
 A/Reference number: JN0364, MUID:85022828, PMID:6689612
 A/Contents: B2 variant
 A/Accession: JN0364
 A/Molecule type: mRNA
 A/Residues: 92-156, 'I', 158-168, 'A', 170-173, 'T', 175-190 <GO2>
 A/Cross-references: GB:M3833; NID:g162806; PIDN:AA30432.1; PID:g162807
 A/Note: the authors translated the codon TTG for residue 100 as Pro and GAA for residue
 R/Mercier, J.C.; Brignon, G.; Ribadeau-Dumas, B.
 Eur. J. Biochem. 35, 222-225, 1973
 A>Title: Structure primaire de la caseine kappa bovine. Sequence complete.
 A/Reference number: A91206, MUID:73216467, PMID:4577852
 A/Contents: B variant
 A/Accession: A91206
 A/Molecule type: protein
 A/Residues: 22-101, 'D', 103-127 <MER>
 A/Note: the amino-terminal residue appears to be pyrrolidone carboxylic acid, but cycliz
 R/Grosclaude, E.; Mahe, M.F.; Mercier, J.C.; Ribadeau-Dumas, B.
 Ann. Genet. Sel. Anim. 4, 515-521, 1972
 A>Title: Localisation des substitutions d'acides amines differentiant les variants A et
 A/Reference number: A90033
 A/Contents: A variant
 A/Accession: A90033
 A/Molecule type: protein
 A/Residues: 128-190 <GRO>
 A/Note: article in French with English abstract
 R/Jolles, J.; Schoentgen, F.; Alaïs, C.; Jolles, P.
 Chimia 26, 645-646, 1972
 A/Reference number: A90920
 A/Contents: A variant
 A/Accession: A90920
 A/Molecule type: protein
 A/Residues: 22, 'Q', 24-25, 'E', 27, 'E', 29-126 <JO2>
 R/Jolles, J.; Schoentgen, F.; Alaïs, C.; Fiat, A.M.; Jolles, P.
 Helv. Chim. Acta 55, 2872-2883, 1972
 A>Title: Studies on the primary structure of cow kappa-casein. Structural features of pa
 A/Reference number: A91634, MUID:73124636, PMID:4653404
 A/Contents: B variant
 A/Accession: A91634
 A/Molecule type: protein
 A/Residues: 22-101, 'D', 103-156, 'I', 158-168, 'A', 170-190 <JO>
 R/Guerin, J.; Alaïs, C.; Jolles, P.; Jolles, P.
 Biochim. Biophys. Acta 351, 325-332, 1974
 A>Title: kappa-casein from bovine colostrum.
 A/Reference number: A90592, MUID:74269749, PMID:4407313
 A/Accession: A90592
 A/Molecule type: protein
 A/Residues: 127-156, 'I', 158-168, 187-190 <GUE>
 A/Experimental source: colostrum
 R/Mercier, J.C.; Uro, J.; Ribadeau-Dumas, B.; Grosclaude, F.
 Eur. J. Biochem. 27, 535-547, 1972
 A>Title: Structure primaire du caseinomacropепptide de la caseine kappa-1 bovine.
 A/Reference number: A60833, MUID:72254481, PMID:455180
 A/Contents: B variant
 A/Accession: A60833
 A/Molecule type: protein
 A/Residues: 128-156, 'I', 158-168, 'A', 170-190 <ME2>
 A/Note: article in French with English abstract
 R/Droese, H.B.; Folmann, B.
 Biochim. Biophys. Acta 95, 221-224, 1989
 A>Title: Specificity of milk-clotting enzymes towards bovine kappa-casein.
 A/Reference number: S03993, MUID:89207571, PMID:2495817
 A/Accession: S03993
 A/Molecule type: protein
 A/Residues: 126-130 <DRO>

R/Gorodetski, S.I.; Kaledin, A.S.
 Genetika 23, 398-404, 1987
 A>Title: Analysis of nucleotide sequence of bovine kappa-casein cna.
 A/Reference number: 145875
 A/Accession: 145875
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-156, 'I', 158-168, 'A', 170-173, 'T', 175-190 <GO3>
 A/Cross-references: GB:M36641, NID:g162810; PIDN:AA30433.1; PID:g162811
 A/Comment: The sequence shown is the A variant.
 C/Genetics:
 A/Introns: 19/3; 30/3
 C/Superfamily: kappa-casein
 C/Keywords: glycoprotein; milk; phosphoprotein
 F.1-21/Domain: signal sequence #status predicted <SIG>
 F.122-190/Product: kappa-casein #status predicted <MAT>
 F.126-127/Cleavage site: Phe-Met (chymosin) #status experimental
 F.152/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F.170/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 41.6%; Score 127; DB 1; Length 190;
 Best Local Similarity 44.4%; Pred. No. 3.4e-07;
 Matches 28; Conservative 7; Mismatches 20; Indels 8; Gaps 1;

QY 1 YORPAAINNPVPRRYANPAVVRPAQIPGRQYFN-----SHPEYVRRPRLH 52
 DB 64 YQGRFVALINNOPLFPYVYAKPAVRSPAQLIQVLSNTVPAKSCAQPTMARHPHPH 123

QY 53 PSF 55
 DB 124 LSF 126

RESULT 6
 KXSA
 kappa-casein precursor - sheep
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 24-Apr-1984 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999
 C/Accession: S14711; A03113; A90597; S08655
 R/Furet, J.P.; Mercier, J.C.; Soulier, S.; Gaye, P.; Hue-Delahaye, D.; Vilotte, J.L.
 Nucleic Acids Res. 18, 5286, 1990
 A>Title: Nucleotide sequence of ovine kappa-casein cDNA.
 A/Reference number: S14711, MUID:90384837, PMID:2402453
 A/Accession: S14711
 A/Molecule type: mRNA
 A/Residues: 1-192 <FUR>
 A/Cross-references: EMBL:X51822; NID:g1293; PIDN:CA36122.1; PID:g1294
 R/Jolles, J.; Schoentgen, F.; Hermann, J.; Alaïs, C.; Jolles, P.
 Eur. J. Biochem. 46, 127-132, 1974
 A>Title: The sequence of sheep kappa-casein: primary structure of para-kappa-A-casein.
 A/Reference number: A91221, MUID:74309256, PMID:4605338
 A/Accession: A03113
 A/Molecule type: protein
 A/Residues: 22, 'Q', 24-27, 'E', 29-129 <JO1>
 R/Jolles, J.; Fiat, A.M.; Schoentgen, F.; Alaïs, C.; Jolles, P.
 Biochim. Biophys. Acta 365, 335-343, 1974
 A>Title: The amino acid sequence of sheep kappa-A-casein. II. Sequence studies concernin
 A/Reference number: A90597, MUID:75036120, PMID:4429673
 A/Accession: A90597
 A/Molecule type: protein
 A/Residues: 127-192 <JO2>
 C/Superfamily: kappa-casein
 C/Keywords: glycoprotein; mammary gland; milk; phosphoprotein
 F.1-21/Domain: signal sequence #status predicted <SIG>
 F.122-192/Product: kappa-casein #status experimental <MAT>

Query Match 40.7%; Score 124; DB 1; Length 192;
 Best Local Similarity 42.9%; Pred. No. 7.5e-07;
 Matches 27; Conservative 6; Mismatches 22; Indels 8; Gaps 1;

QY 1 YORPAAINNPVPRRYANPAVVRPAQIPGRQYFN-----HPEYVRRPRLH 52
 DB 64 YQGRFVALINNOPLFPYVYAKPAVRSPAQLIQVLSNTVPAKSCAQPTMARHPHPH 123

R;Deutch, C.E.; Minicov, I.
Plant Mol. Biol. 27, 411-418, 1995
A;Title: Post-transcriptional regulation of a salt-inducible alfalfa gene encoding a put
A;Reference number: S52985; MUID:95195167; PMID:7886629
A;Accession: S52985
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <DEU>
A;Cross-references: EMBL:L37017; NID:G3818415; PIDN:AMD03487.1; PID:G3818416
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 22.3%; Score 68; DB 2; Length 381;
Best Local Similarity 32.1%; Pred. No. 3.2;
Matches 17; Conservative 10; Mismatches 16; Indels 10; Gaps 3;

QY 5 PAIAINNPYPTTYANPAVVRPAQIPQRYLPNSHP---PTVVRPRLAP 53
Db 156 PVVVPVPPVPRK---PVPVRP-PVVPKPPVVPVPPVVPKPPVIVKPIVFP 202

RESULT 12
AB2067
hypothetical protein al12088 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB2067
R;Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Matenabe, A.; Iritaguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11758940
A;Accession: AB2067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAW73787.1; PID:G17131179; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al12088

Query Match 21.3%; Score 65; DB 2; Length 289;
Best Local Similarity 42.1%; Pred. No. 5.2;
Matches 16; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 4 RPAIAINNPYPTTYANPAVVRPAQIPQRYLPNSH 41
Db 116 RGRIGIFN---RSYYEELLVAVHPEILKQQLPHNH 149

RESULT 13
S23760
polymenolic adhesive protein 1 [validated] - blue mussel (fragment)
N;Alternate names: MAFP-1
C;Species: Mytilus edulis (blue mussel)
C;Date: 27-May-1994 #sequence_revision 10-Nov-1995 #text_change 02-Jun-2000
C;Accession: S23760; A59158; K20840
R;Filipula, D.R.; Lee, S.M.; Link, R.P.; Strausberg, S.L.; Strausberg, R.L.
Biotechnol. Prog. 6, 171-177, 1990
A;Title: Structural and functional repetition in a marine mussel adhesive protein.
A;Reference number: S23760; MUID:91025829; PMID:1367451
A;Accession: S23760
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-875 <FIL>
A;Cross-references: EMBL:X54422; NID:G9695; PID:G9696
R;Taylor, S.W.; Waite, J.H.; Ross, M.M.; Shabanowitz, J.; Hunt, D.F.
J. Am. Chem. Soc. 116, 10803-10804, 1994
A;Title: trans-2,3-cis-3,4-dihydroxyproline, a new naturally occurring amino acid, is th
A;Reference number: A59158
A;Accession: A59158
A;Molecule type: protein
A;Residues: 173-182 <TA>

A;Note: this peptide is the consensus tandem repeat decapeptide
R;Waite, J.H.
J. Biol. Chem. 258, 2911-2915, 1983
A;Title: Evidence for a repeating 3,4-dihydroxyphenylalanine- and hydroxyproline-contai
A;Reference number: A20840; MUID:83135732; PMID:6298211
A;Accession: A20840
A;Molecule type: protein
A;Residues: 173-182 <WA>
C;Keywords: hydroxyproline; tandem repeat
F;59,115,145,155,175,185,195,211,221,237,247,257,285,295,305,315,325,335,351,361,371,387
3/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;91,95,117,121,147,151,157,161,177,181,187,191,197,201,213,217,223,227,239,243,249,253
/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F;92,118,148,158,178,188,198,211,224,240,250,260,288,298,308,318,328,338,354,364,374,391
6/Modified site: trans-2,3-cis-3,4-dihydroxyproline (Pro) #status experimental
F;93,149,159,179,189,199,225,241,251,261,289,299,309,319,329,339,365,375,391,401,411,437
hydroxyproline (Pro) #status experimental
F;435,439,445,449,461,465,471,475,481,485,521,525,541,545,551,555,561,565,571,575,581,587
59/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
F;765,769,775,779,815,819,835,839,865,869/Modified site: 3',4'-dihydroxyphenylalanine (T
F;766,776,816,836,866/Modified site: trans-2,3-cis-3,4-dihydroxyproline (Pro) #status ex
F;813,833/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

Query Match 21.3%; Score 65; DB 2; Length 875;
Best Local Similarity 27.1%; Pred. No. 18;
Matches 19; Conservative 10; Mismatches 23; Indels 18; Gaps 3;

QY 1 YORPAAINNPYPTTYANPAVVRPAQIPQRYLPN-----SHPTV 45
Db 95 YKSKPTVPKXTY--PPTVAKPSY--PSSYKPKTYPTYPKTYPTYPKPSYPTV 151

QY 46 VRPRLHPSPF 55
Db 152 KPKPSYPSY 161

RESULT 14
TS2359
hypothetical protein B11E.80 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: TS2359
R;Schulte, U.; Algen, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, September 2000
A;Reference number: Z26053
A;Accession: TS2359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1400 <SCH>
A;Cross-references: EMBL:AL442043; GSPDB:GN00116; NCSP:B11E.80
A;Experimental source: BAC clone B11E; strain OR74A
C;Genetics:
A;Gene: NCSP:B11E.80
A;Map position: 6

Query Match 21.3%; Score 65; DB 2; Length 1400;
Best Local Similarity 37.5%; Pred. No. 29;
Matches 24; Conservative 5; Mismatches 23; Indels 12; Gaps 4;

QY 2 QRPAAINNPYPTTYANPAV--VRPAQI-----PQRYLP---NSPPTVVR-RP 49
Db 1138 QRPRQGGSGGGLPPLQPNPILQPPRPAQIQPRPQPLRPPQLRQPLQKQPPTRLP 1197

QY 50 NLAP 53
Db 1198 QLLP 1201

RESULT 15
T55073
hypothetical protein T21C9.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25073
R:McMurray, A.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19977
A:Accession: T25073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-254 <MT>
A:Cross-references: EMBL:Z73098; PIDN:CAA97336.1; GSPDB:GN00023; CESP:T21C9.9
A:Experimental source: clone T21C9
C:Genetics:
A:Gene: CESP:T21C9.9
A:Map position: 5
A:Introns: 22/2; 78/3

Query Match 21.1%; Score 64.5; DB 2; Length 254;
Best Local Similarity 28.6%; Pred. No. 5.1;
Matches 18; Conservative 9; Mismatches 21; Indels 15; Gaps 3;
QY 1 YORRPAIANNPYPRVYANPAVWPHAQIFQOYL PNS-----HPPTVVRPNL 51
Db 79 YQGPRAGSLQQWY---QLNPRYIQP--QAPRPQYISRPAAPAPAPYQPPRVQGRPYV 132
QY 52 HPS 54
Db 133 QPA 135

Search completed: September 1, 2004, 00:17:04
Job time: 34.9 secs

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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:44 ; Search time 18.7 Seconds

(without alignments)
153.148 Million cell updates/sec

Title: US-09-508-095-17

Perfect score: 305

Sequence: 1 YORRPAIATNPNYPRTYYA.....YLPNSHPPTVVRNPLPSPF 55

Scoring table: BLOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Swissprot_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	100.0	182	1	CASK_HUMAN
2	187	61.3	135	1	CASK_EOGR
3	186	61.0	145	1	CASK_BALPH
4	183	60.0	185	1	CASK_HORSE
5	181	59.3	146	1	CASK_TAPIN
6	181	59.3	146	1	CASK_UNCUN
7	171	56.1	145	1	CASK_HIPAM
8	165	54.1	125	1	CASK_LAMGU
9	165	54.1	182	1	CASK_CAMDR
10	160	52.5	146	1	CASK_TAYTA
11	160	52.5	188	1	CASK_PIG
12	135	44.3	190	1	CASK_BUBBU
13	134	43.9	192	1	CASK_OREAM
14	129	42.3	192	1	CASK_CAPCR
15	129	42.3	192	1	CASK_CAPI
16	129	42.3	192	1	CASK_CAPSU
17	129	42.3	192	1	CASK_CAPSW
18	129	42.3	192	1	CASK_NEMCO
19	129	42.3	202	1	CASK_SAITA
20	127	41.6	136	1	CASK_BISBO
21	127	41.6	190	1	CASK_BOVIN
22	124	40.7	192	1	CASK_RUPRU
23	124	40.7	192	1	CASK_SHEEP
24	121	39.7	190	1	CASK_CERNT
25	120	39.3	153	1	CASK_GIRCA
26	119	39.0	150	1	CASK_RABIT
27	114	37.4	171	1	CASK_TAJUA
28	114	36.4	122	1	CASK_CERUN
29	111	36.4	122	1	CASK_CERUN
30	106	34.8	124	1	CASK_OVIMO
31	103	33.8	122	1	CASK_ELADA
32	103	33.8	122	1	CASK_ODOHE
33	103	33.8	122	1	CASK_ODOVI

34	103	33.8	122	1	CASK_RANTA	O95239 rangifer ta
35	101	33.1	124	1	CASK_OVIDA	O95224 ovis dalli
36	100	32.8	122	1	CASK_MUNRE	O95199 muntiacus r
37	99	32.5	122	1	CASK_CEREL	O95149 cervus elap
38	99	32.5	123	1	CASK_CAPCA	O95146 capreolus c
39	95	31.1	122	1	CASK_MAZAM	O95191 mazama amer
40	93	30.5	234	1	CASK_CAVPO	P19442 cavia porce
41	72.5	23.8	872	1	FPI_MYTCC	O25434 mytilus cor
42	69.5	22.8	340	1	LRII_HSYAF	P17588 herpes simp
43	65	22.6	728	1	TREB_NEUCR	O42783 neurospora
44	65	21.3	875	1	FPI_MYTEO	O25460 mytilus edu
45	64.5	21.1	735	1	TREB_SCHPO	O42893 schizosacch

ALIGNMENTS

RESULT 1	CASK_HUMAN	STANDARD:	PRT:	182 AA.
AC	P07498; 013575;			
DT	01-APR-1998 (Rel. 07, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Kappa casein precursor.			
GN	CSN3 OR CSN10 OR CSNK OR CASK.			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_Taxid=9606;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Menon R.S., Jeffers K.F., Chang Y.F., Ham R.G.;			
RL	submitted (xxx-1991) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=93208373; PubMed=1296818;			
RA	Bergstrom S., Hansson L., Herneli O., Loennertal B., Nilsson A.K.,			
RL	Strengvist M.;			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97017129; PubMed=8863730;			
RA	Edlund A., Johansson T., Leidvik B., Hansson L.;			
RL	"Structure of the human kappa-casein gene.";			
RN	Gene 174:65-69 (1996).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RL	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RL	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,			
RL	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.C., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,			
RL	Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RL	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RL	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RL	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,			
RL	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalite D.E.,			
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.;			
RL	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences".			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[15]			


```

CC CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
OC Balaenopteridae; Balaenoptera.  
OX NCBI_taxid=9770;  
RN  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96364219; PubMed=8752004;  
RX Ganesy J., Hayashi C., Cronin M.A., Arcander P.;  
RT "Evidence from milk casein genes that cetaceans are close relatives  
of hipopotamids artiodactyls."  
RL Mol. Biol. Evol. 13:954-963(1996).  
CC -I- FUNCTION: Kappa casein stabilizes micelle formation, preventing  
casein precipitation in milk.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Mammary gland specific; secreted in milk.  
CC -I- SIMILARITY: Belongs to the kappa-casein family.  
-----  
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or send an email to license@isb-stb.ch).  
-----  
DR EMBL; U53888; AAB08404.1; -.  
DR InterPro; IPR000117; Casein_kappa.  
DR Pfam; PF00097; Casein_kappa.1.  
DR ProDom; PD003689; Casein_kappa.1.  
KM Milk; Phosphorylation; Glycoprotein.  
FT NON_TER 1 82 CLEAVAGE (BY CHYMOSIN (=RENNIN))  
FT SITE 1 82 (BY SIMILARITY).  
SQ SEQUENCE 145 AA; 16324 MW; 17024F195BA78781 CRC64;  
  
Query Match 61.0%; Score 186; DB 1; Length 145;  
Best Local Similarity 61.8%; Pred.No. 2.1e-14;  
Matches 34; Conservative 4; Mismatches 17; Indels 0; Gaps 0,  
  
OY 1 YQRRPAILNPPYPVRYTYANPAVVAPRPAIQIPQRQYLPNSSHPTVRARNLPSPF 55  
DB 27 YQHRLAALINNQFMPEPYAKRVAAHPHQAIRIQMQLFNHNHPVTAAHHPHRPSF 81  
  
RESULT 4  
CASK_HORSE  
ID AC P82187; O8SPRO; STANDARD; PRT; 185 AA.  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Kappa casein precursor (Kappa-CN).  
GN CSN3 OR CSN10.  
DS Equus caballus (Horse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Perissodactyla; Equidae; Equus.  
OX NCBI_taxid=9796;  
RN  
RP SEQUENCE FROM N.A.  
RA MEDLINE=22504255; PubMed=12617290;  
RX Lénassi T., Rogeli I., Dovc P.;  
RT "Characterization of equine cDNA sequences for alphaS1-, beta- and  
kappa-casein".  
RL J. Dairy Res. 70:29-36(2003).  
RN [2]  
RP SEQUENCE OF 21-181.  
RC TISSUE=Milk;  
RU Tedeschi G.;  
RT Submitted (NOV-1999) to Swiss-Prot.  
CC -I- FUNCTION: Kappa casein stabilizes micelle formation, preventing  
casein precipitation in milk.  
CC -I- SUBCELLULAR LOCATION: Secreted.
```

```

CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC -1- SIMILARITY: Belongs to the kappa-casein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY040863; AAK83669.1; -
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
KW Milk; Phosphorylation; Signal.
FT SIGNAL 1 20
FT CHAIN 21 185
FT SITE 117 118
FT -----
FT CONFLICT 29 34
FT CONFLICT 112 112
FT CONFLICT 152 152
FT SEQUENCE 185 AA; 21021 MM; F7634PF52CEB30606 CnC64;
SQ
Query Match 60.0%; Score 183; DB 1; Length 185;
Best Local Similarity 63.6%; Pred. No. 6,1e-14;
Matches 35; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
OY 1 YORPAPALINNPYKRTYANPAVRRHACIPOKQOYVPSNHSRPRVRRPNLPSF 55
Db 63 YQHLALINQHPQYIYKAPPAARPAVRQIPIQVQVLPNTYPSIVRRHCPSPF 117
-----
RESULT 5
CASK_TAPIN STANDARD; PRT; 146 AA.
ID CASK_TAPIN
AC Q29135.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kappa casein (Fragment).
DE CSN3 OR CSN10 OR CSN8.
GN Tapirus indicus (Asiatic tapir) (Malayan tapir)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID:9802;
[1]
SEQUENCE FROM N.A.
MEDLINE=96364219; PubMed=8752004;
Gatesy J., Hayaashi C., Cronin M.A., Arcander P.,
"Evidence from milk casein genes that cetaceans are close relatives
of hippopotamid artiodactyls.",
Mol. Biol. Evol. 13:954-963(1996).
-1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
casein precipitation in milk.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
-1- SIMILARITY: Belongs to the kappa-casein family.
CC -----
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CC -----
DR EMBL; U53892; AAB08418.1; -
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; Casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
KW Milk; Phosphorylation; Glycoprotein.

```

FT NON TER 1 1
 FT SITE 80 81 CLEAVAGE (BY CHYMOSIN (=RENNIN))
 FT SEQUENCE 146 AA; 16691 MW; E8957001E0B85CF CRC64;
 (BY SIMILARITY)

Query Match 59.3%; Score 181; DB 1; Length 146;
 Best Local Similarity 61.8%; Pred. No. 7.9e-14;
 Matches 34; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 YORRPALAINNPVPTTYANPAVVRPHQIPQRYLPNSHPTVVRPNLHPSF 55
 DB 27 YORRPVAVINQOMPYRYAPVAPVPHQIPQWOLVPLVPTVVRPHRPSF 81

RESULT 6

CASK_UNCUN STANDARD; PRT; 146 AA.

AC Q29150;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kappa casein (Fragment).
 OS CSN3 OR CSN10 OR CSNK.
 GN Uncia uncia (Snow Leopard) (Panthera uncia).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Uncia.
 OX NCBI_TaxID=29064;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96364219; PubMed=8752004;
 RA Gatesy J., Hayashi C., Cronin M.A., Arcander P.;
 RT "Evidence from milk casein genes that cetaceans are close relatives
 of hippopotamid artiodactyls.";
 RL Mol. Biol. Evol. 13:954-963(1996).
 CC -1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
 casein precipitation in milk.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
 CC -1- SIMILARITY: Belongs to the kappa-casein family.
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DR EMBL; U53894; AAB08421.1; -
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR ProDom; PD003689; Casein_kappa.1.
 KW Milk; Phosphorylation; Glycoprotein.
 FT NON TER 1
 SQ SEQUENCE 146 AA; 16337 MW; D667DEDF607E5B66 CRC64;

Query Match 59.3%; Score 181; DB 1; Length 146;
 Best Local Similarity 58.2%; Pred. No. 7.9e-14;
 Matches 32; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 YORRPALAINNPVPTTYANPAVVRPHQIPQRYLPNSHPTVVRPNLHPSF 55
 DB 27 YORRPVAVINQOMPYRYAPVAPVPHQIPQWOLVPLVPTVVRPHRPSF 81

RESULT 7

CASK_HIPAM STANDARD; PRT; 145 AA.

AC Q28441;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kappa casein (Fragment).

GN CSN3 OR CSN10 OR CSNK.
 OS Hippopotamus amphibius (Hippopotamus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Hippopotamidae; Hippopotamus.
 OX NCBI_TaxID=9833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96364219; PubMed=8752004;
 RA Gatesy J., Hayashi C., Cronin M.A., Arcander P.;
 RT "Evidence from milk casein genes that cetaceans are close relatives
 of hippopotamid artiodactyls.";
 RL Mol. Biol. Evol. 13:954-963(1996).
 CC -1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
 casein precipitation in milk.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
 CC -1- SIMILARITY: Belongs to the kappa-casein family.

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DR EMBL; U53894; AAB08413.1; -
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR ProDom; PD003689; Casein_kappa.1.
 KW Milk; Phosphorylation; Glycoprotein.
 FT NON TER 1
 FT CARBOHYD 91
 SQ SEQUENCE 145 AA; 16272 MW; 874A9EEFDF80398 CRC64;

Query Match 56.1%; Score 171; DB 1; Length 145;
 Best Local Similarity 60.0%; Pred. No. 1.1e-12;
 Matches 33; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 YORRPALAINNPVPTTYANPAVVRPHQIPQRYLPNSHPTVVRPNLHPSF 55
 DB 27 YORRPALAINNPVPTTYANPAVVRPHQIPQWOLVPLVPTVVRPHRPSF 81

RESULT 8

CASK_LAMGU STANDARD; PRT; 125 AA.

AC Q28451;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kappa casein (Fragment).
 OS CSN3 OR CSN10 OR CSNK.
 GN Lama guanicoe (Guanaco).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9840;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96364219; PubMed=8752004;
 RA Gatesy J., Hayashi C., Cronin M.A., Arcander P.;
 RT "Evidence from milk casein genes that cetaceans are close relatives
 of hippopotamid artiodactyls.";
 RL Mol. Biol. Evol. 13:954-963(1996).
 CC -1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
 casein precipitation in milk.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
 CC -1- SIMILARITY: Belongs to the kappa-casein family.

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RC TISSUE=Mammary gland;
RX MEDLINE=92367959; PubMed=1503275;
RA Levine W.B., Alexander L.J., Hoganson G.E., Beattie C.W.;
RT "Cloning and sequencing of the porcine kappa-casein cDNA.";
RL Anim. Genet. 23:361-363(1992).
RN [2]
RP SEQUENCE OF 118-188.
RX MEDLINE=77068846; PubMed=1001463;
RA Crobert J.M., Mercier J.-C., Baby C., Haze G.;
RT "Primary structure of the casein macropeptide of porcine and human
  kappa caseins.";
RL FEBS Lett. 72:173-178(1976).
CC -1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
  casein precipitation in milk.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC -1- SIMILARITY: Belongs to the kappa-casein family.
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CC -----
DR EMBL/ X51977; CA36239.1; -.
DR PIR/ A48382; A48382.
DR InterPro/ IPR000117; Casein_kappa.
DR Pfam/ PF00997; Casein_kappa.1.
DR ProDom/ PD003689; Casein_kappa.1.
KW Milk; Glycoprotein; Phosphorylation; Signal.
FT SIGNAL 1 21
FT CHAIN 22 188
FT SITE 117 118
FT SITE 117 118
SQ SEQUENCE 188 AA; 21122 MW; 9B41EB19B5D36A CRC64;

Query Match 52.5%; Score 160; DB 1; Length 188;
Best Local Similarity 54.5%; Pred. No. 2.5e-11;
Matches 30; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 YQRRPALINNPVPTTYANPAVAPVPHQIPQRCYLNSHPPTVRRPNLHPSF 55
Db 63 YQHRSAVSPRQPIFYPAVPAVPAHQAQKQWQDPVPPVARRPRPHASF 117

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RT buffalo.
RL Biochimie 59:375-379(1977).
CC -1- FUNCTION: Kappa casein stabilizes micelle formation, preventing
  casein precipitation in milk.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC -1- SIMILARITY: Belongs to the kappa-casein family.
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CC -----
DR EMBL/ D14370; BAA03285.1; -.
DR EMBL/ D14368; BAA03285.1; JOINED.
DR EMBL/ D14369; BAA03285.1; JOINED.
DR InterPro/ IPR000117; Casein_kappa.
DR Pfam/ PF00997; casein_kappa.1.
DR ProDom/ PD003689; Casein_kappa.1.
KW Milk; Phosphorylation; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 190
FT SITE 126 127
FT SITE 126 127
FT CARBOHYD 152 152
FT MOD_RES 170 170
FT VARIANT 156 156
FT VARIANT 172 172
SQ SEQUENCE 190 AA; 21397 MW; EE858824628A96AD CRC64;

Query Match 44.3%; Score 135; DB 1; Length 190;
Best Local Similarity 46.0%; Pred. No. 1.7e-08;
Matches 29; Conservative 7; Mismatches 19; Indels 8; Gaps 1;

QY 1 YQRRPALINNPVPTTYANPAVAPVPHQIPQRCYLNSHPPTVRRPNLHPSF 52
Db 64 YQKRPVALINNGFLPYPAVPAVPAHQAQKQWQDPVPPVARRPRPHASF 123

RESULT 12
CASK_BUBBU STANDARD; PRT; 190 AA.
ID CASK_BUBBU
AC P11840;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kappa casein precursor.
GN CSN3 OR CSN10 OR CSNK.
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96139018; PubMed=8587130;
RA Chikuni K., Mori Y., Tabata T., Saito M., Momma M., Kosugiama M.;
RT "Molecular phylogeny based on the kappa-casein and cytochrome b
  sequences in the mammalian suborder Ruminantia.";
RL J. Mol. Evol. 41:859-866(1995).

RESULT 13
CASK_OREAM STANDARD; PRT; 192 AA.
ID CASK_OREAM
AC P50423;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kappa casein precursor.
GN CSN3 OR CSN10 OR CSNK.
OS Oreamnos americanus (Mountain goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Oreamnos.
OX NCBI_TaxID=34873;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96139018; PubMed=8587130;
RA Chikuni K., Mori Y., Tabata T., Saito M., Momma M., Kosugiama M.;
RT "Molecular phylogeny based on the kappa-casein and cytochrome b
  sequences in the mammalian suborder Ruminantia.";
RL J. Mol. Evol. 41:859-866(1995).

RP SEQUENCE OF 69-192 FROM N.A.
RX MEDLINE=97055443; PubMed=8899730;
RA Cronin M.A., Stuart R., Pierson B.J., Patton J.C.;
RT "K-casein gene phylogeny of higher ruminants (Pecora, Artiodactyla).";
RL Mol. Phylogenet. Evol. 6:295-311(1996).

```

```

CC - FUNCTION: Kappa casein stabilizes micelle formation, preventing
CC casein precipitation in milk.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC - SIMILARITY: Belongs to the kappa-casein family.
-----
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-----
DR EMBL; D32185; BAA06886.1; -.
DR EMBL; D32183; BAA06886.1; JOINED.
DR EMBL; D32184; BAA06886.1; JOINED.
DR EMBL; U37512; AAC48658.1; -.
DR InterPro: IPR000117; Casein_kappa.
DR Pfam: PF00997; Casein_kappa.1.
DR ProDom: PD003689; Casein_kappa.1.
KW Milk; Phosphorylation; Glycoprotein; Signal;
KW Pyroglutamate carboxylic acid.
FT FT SIGNAL 1 21
FT CHAIN 22 192
FT SITE 126 127
FT MOD_RES 22 22
FT CARBOHYD 152 152
FT MOD_RES 172 172
FT MOD_RES 189 189
SQ SEQUENCE 192 AA; 21525 MW; 95BA346766DD402A CRC64;

Query Match 43.9%; Score 134; DB 1; Length 192;
Best Local Similarity 46.0%; Pred. No. 2.3e-08;
Matches 29; Conservative 6; Mismatches 20; Indels 8; Gaps 1;

QY 1 YORRPAIINNPVPTTYANPAVVRPHAQIPQROYLPNS-----HPPTVRRPNLH 52
DB 64 YQQRVAILNNQFLPYFYAKVAVRSPAQILQMOVLPNTVPAKSCQDPTTMAHHPH 123

QY 53 PSF 55
DB 124 LSF 126

RESULT 14
CASK_CAPCR STANDARD; PRT; 192 AA.
ID CASK_CAPCR
AC P42156;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kappa casein precursor.
GN CSN3 OR CSN10 OR CSNK.
OS Capricornis capripus (Japanese serow).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capricornis.
OX NCBI_TaxID=9966;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96139018; PubMed=8587130;
RA Chikuni K., Mori Y., Tabata T., Saito M., Momma M., Kosugiya M.;
RT "Molecular phylogeny based on the kappa-casein and cytochrome b
RT sequences in the mammalian suborder Ruminantia.",
RL J. Mol. Evol. 41:859-866(1995).
CC - FUNCTION: Kappa casein stabilizes micelle formation, preventing
CC casein precipitation in milk.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC - SIMILARITY: Belongs to the kappa-casein family.

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CC - FUNCTION: Kappa casein stabilizes micelle formation, preventing
CC casein precipitation in milk.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC - SIMILARITY: Belongs to the kappa-casein family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; D14376; BAA03287.1; -.
DR EMBL; D14374; BAA03287.1; JOINED.
DR EMBL; D14375; BAA03287.1; JOINED.
DR InterPro: IPR000117; Casein_kappa.
DR Pfam: PF00997; Casein_kappa.1.
DR ProDom: PD003689; Casein_kappa.1.
KW Milk; Phosphorylation; Glycoprotein; Signal;
KW Pyroglutamate carboxylic acid.
FT FT SIGNAL 1 21
FT CHAIN 22 192
FT SITE 126 127
FT MOD_RES 22 22
FT CARBOHYD 152 152
FT MOD_RES 172 172
FT MOD_RES 189 189
FT VARIANT 8 8
SQ SEQUENCE 192 AA; 21486 MW; 1261CB4DB1AE9AC CRC64;

Query Match 42.3%; Score 129; DB 1; Length 192;
Best Local Similarity 44.4%; Pred. No. 8.4e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 8; Gaps 1;

QY 1 YORRPAIINNPVPTTYANPAVVRPHAQIPQROYLPNS-----HPPTVRRPNLH 52
DB 64 YQQRVAILNNQFLPYFYAKVAVRSPAQILQMOVLPNTVPAKSCQDPTTMAHHPH 123

QY 53 PSF 55
DB 124 LSF 126

RESULT 15
CASK_CAPHI STANDARD; PRT; 192 AA.
ID CASK_CAPHI
AC P02670; Q8SPW9; Q8SPN0; Q8SPV1; Q8SPW6; Q8SPW8; Q8MWV5;
AC O8MW74;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kappa casein precursor (Kappa-CN).
GN CSN3 OR CSN10 OR CSNK.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ssp. aegagrus; TISSUE=Mammary gland;
RX MEDLINE=94042560; PubMed=8226388;
RA Coll A., Polch J.M., Sanchez A.;
RT "Nucleotide sequence of the goat kappa-casein cDNA.",
RL J. Anim. Sci. 71:2833-2833(1993).
CC - FUNCTION: Kappa casein stabilizes micelle formation, preventing
CC casein precipitation in milk.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
CC - SIMILARITY: Belongs to the kappa-casein family.

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DR InterPro:IPR000117; Casein_kappa.
DR Pfam: PF00997; casein_kappa.1.
DR ProDom: PD003689; Casein_kappa.1.
KW Milk; phosphorylation; glycoprotein; Signal; Polymorphism;
KW Pyrolydione carboxylic acid.
FT SIGNAL 1 21
FT CHAIN 1 192
FT SITE 126 127
FT MOD_RES 22 22
FT MOD_RES 172 172
FT MOD_RES 189 189
FT VARIANT 65 65
FT VARIANT 86 86
FT VARIANT 111 111
FT VARIANT 140 140
FT VARIANT 177 177
FT VARIANT 180 180
FT CONFLICT 134 134
FT SEQUENCE 192 AA; 21441 MW; 009F558F4BE3178 CRC64;
SQ
Query Match 42.3%; Score 129; DB 1; Length 192;
Best Local Similarity 44.4%; Pred. No. 8.4e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 8; Gaps 1
OY 1 YQRRPALINNNYVVRTIYANPAVYRPFNAQIPQGYLPNS-----HPETVRRSNLH 52
Db 64 YQRRPALINNNFLPYPAKRVAVRSPAQTLQWQVLPNTVPKASCODQPTLARRBHPH 123
OY 53 PSF 55
Db 124 LSF 126

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:56:54 ; Search time 101.933 Seconds
(without alignments)
170.244 Million cell updates/sec

Title: US-09-508-095-17
Perfect score: 305
Sequence: 1 YQRRPALAINNPYVPRITYA.....YLPNSHPPTVVRPNLHPGF 55

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218	71.5	146	6	P79091
2	207	67.9	145	6	Q865E0
3	207	67.9	145	6	Q865D9
4	207	67.9	145	6	Q865D8
5	207	67.9	145	6	Q865D6
6	207	67.9	145	6	Q865D5
7	207	67.9	145	6	Q865D4
8	207	67.9	145	6	Q865D3
9	207	67.9	145	6	Q865D2
10	207	67.9	145	6	Q865D1
11	207	67.9	145	6	Q865D0
12	207	67.9	145	6	Q861U4
13	207	67.9	145	6	Q861U3
14	207	67.9	145	6	Q861T9
15	207	67.9	145	6	Q861T8
16	207	67.9	145	6	Q861T7

17	206	67.5	145	6	Q865D7	Q865D7	ursus arcto
18	192	63.0	145	6	Q865D4	Q865D4	delphinidae
19	187	61.3	145	6	P79230	P79230	physeter ca
20	131	43.0	90	6	Q95MY5	Q95MY5	canchohaete
21	129	42.3	159	6	Q86N75	Q86N75	capra hircu
22	129	42.3	162	6	Q7YRV1	Q7YRV1	capra ibex
23	129	42.3	162	6	Q7YRU9	Q7YRU9	capra sibir
24	128	42.0	162	6	Q7YRX5	Q7YRX5	capra hircu
25	128	42.0	162	6	Q7YRX3	Q7YRX3	capra hircu
26	127	41.6	160	6	Q9N1F1	Q9N1F1	bos mutus g
27	127	41.6	160	6	Q9N273	Q9N273	bos indicus
28	127	41.6	164	6	Q86MR2	Q86MR2	bos mutus g
29	127	41.6	164	6	Q86MR3	Q86MR3	bos mutus g
30	125	41.0	162	6	Q7YRX4	Q7YRX4	capra hircu
31	124	40.7	125	6	Q95098	Q95098	antilocapra
32	124	40.7	141	6	Q86X10	Q86X10	alces alces
33	124	40.7	160	6	Q9N258	Q9N258	bos taurus
34	124	40.7	162	6	Q7YRV2	Q7YRV2	capra hircu
35	123	40.3	90	6	Q95M22	Q95M22	syncerus ca
36	123	40.3	90	6	Q95MY6	Q95MY6	alcelaphus
37	121	39.7	90	6	Q95MY8	Q95MY8	raphicerus
38	121	39.7	90	6	Q95MX7	Q95MX7	raphicerus
39	121	39.7	141	6	Q86XG4	Q86XG4	capreolus c
40	120	39.3	162	6	Q7YRX2	Q7YRX2	capra hircu
41	118	38.7	90	6	Q95MX4	Q95MX4	oreotragus
42	118	38.7	162	6	Q7YRV0	Q7YRV0	capra sibir
43	117	38.4	90	6	Q95MY7	Q95MY7	batragus h
44	117	38.4	90	6	Q95M20	Q95M20	oryx gazell
45	117	38.4	90	6	Q95MY0	Q95MY0	antidorcas

ALIGNMENTS

RESULT 1	P79091	PRELIMINARY;	PRT;	146 AA.
ID	P79091			
AC	P79091			
DT	01-MAY-1997 (TRENBLREL. 03, Created)			
DT	01-MAY-1997 (TRENBLREL. 03, Last sequence update)			
DT	01-JUN-2003 (TRENBLREL. 24, Last annotation update)			
DE	Kappa casein (Fragment).			
OS	Allurus fulgens (Lesser panda).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.			
OX	NCBI_TaxID=9649;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gatesy J.			
RT	"More DNA support for a Cetacea/Hippopotamidae clade: the blood			
RT	clotting protein gene g-fibrinogen."			
RI	Mol. Biol. Evol. 0:0-0(1997).			
DR	EMBL; U8645; AB47431.1; .			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	InterPro; IPR000117; Casein_kappa.			
DR	Pfam; PF00997; casein_kappa; 1.			
DR	ProDom; PD003689; Casein_kappa; 1.			
FT	NON_TER			
SQ	SEQUENCE 146 AA; 16478 MW; 069878C81CCAB45 CRC64;			
Query Match	71.5%; Score 218; DB 6; Length 146;			
Best Local Similarity	69.1%; Pred. No. 3.3e-19;			
Matches	38; Conservative 6; Mismatches 11; Indels 0; Gaps 0;			
Qy	1 YQRRPALAINNPYVPRITYANPAVPPHAQIPQRYLPNSHPPTVVRPNLHPGF 55			
Db	27 YSHRPVAVINHQVPPYPAKPAVIRPHACIPQVLPNAVPPVVRPNLHPGF 81			
RESULT 2	Q865E0	PRELIMINARY;	PRT;	145 AA.
ID	Q865E0			
AC	Q865E0			

DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus americanus (American black bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB590_6;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF439903; AAO63786.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR InterPro: IPR000117; Casein_kappa.
 DR Pfam: PF00997; casein_kappa.1.
 DR ProDom: PD003689; Casein_kappa.1.
 FT NON TER 1 145
 FT SEQUENCE 145 AA; 16210 MW; 3538009BA8269A0F CRC64;
 SQ

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORPATAINNPYPRTYANPAVVRPAAQIPORQYLPNSHPPTVVRPNLHPSF 55
 DB 27 YPHRPAPVPHNQVVPYVYAKPAVAVRPYQIPQWQVLPNAVYPTTVVHRPHLHPSF 81

RESULT 3

Q865D9 PRELIMINARY; PRT; 145 AA.
 ID Q865D9
 AC Q865D9;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus arctos (Brown bear) (Grizzly bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GK20_9;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF439906; AAO63789.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR InterPro: IPR000117; Casein_kappa.
 DR Pfam: PF00997; casein_kappa.1.
 DR ProDom: PD003689; Casein_kappa.1.
 FT NON TER 1 145
 FT SEQUENCE 145 AA; 16210 MW; 3538009BA8269A0F CRC64;
 SQ

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORPATAINNPYPRTYANPAVVRPAAQIPORQYLPNSHPPTVVRPNLHPSF 55
 DB 27 YPHRPAPVPHNQVVPYVYAKPAVAVRPYQIPQWQVLPNAVYPTTVVHRPHLHPSF 81

RESULT 4
 Q865D8 PRELIMINARY; PRT; 145 AA.

AC Q865D8;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus arctos (Brown bear) (Grizzly bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GK4_7;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF439908; AAO63790.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR InterPro: IPR000117; Casein_kappa.
 DR Pfam: PF00997; casein_kappa.1.
 DR ProDom: PD003689; Casein_kappa.1.
 FT NON TER 1 145
 FT SEQUENCE 145 AA; 16253 MW; 3538109AAB3C30F CRC64;
 SQ

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORPATAINNPYPRTYANPAVVRPAAQIPORQYLPNSHPPTVVRPNLHPSF 55
 DB 27 YPHRPAPVPHNQVVPYVYAKPAVAVRPYQIPQWQVLPNAVYPTTVVHRPHLHPSF 81

RESULT 5

Q865D6 PRELIMINARY; PRT; 145 AA.
 ID Q865D6
 AC Q865D6;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus americanus (American black bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MTB2_4;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF439914; AAO63795.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR InterPro: IPR000117; Casein_kappa.
 DR Pfam: PF00997; casein_kappa.1.
 DR ProDom: PD003689; Casein_kappa.1.
 FT NON TER 1 145
 FT SEQUENCE 145 AA; 16218 MW; 35381D7FCB3CB30F CRC64;
 SQ

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORPATAINNPYPRTYANPAVVRPAAQIPORQYLPNSHPPTVVRPNLHPSF 55
 DB 27 YPHRPAPVPHNQVVPYVYAKPAVAVRPYQIPQWQVLPNAVYPTTVVHRPHLHPSF 81

RESULT 6
 Q865D5

ID Q865D5 PRELIMINARY; PRT; 145 AA.
 AC Q865D5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Kappa casein (Fragment)
 DE Ursus arctos (Brown bear) (Grizzly bear)
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9644;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=SAK7.17;
 RC Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439922; AAC63798.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR Prodom; PD003689; Casein_kappa.1.
 FT NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16291 MW; 3FE4A75963CB313 CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRAPAIINNPYPRTYANPAVVRPHAOIPROQYLPNSHPPTVVRPRLHPSF 55
 DB 27 YHRPAVPIHQYVPPYAKVAVRPYAOIPQOVLPNAPPTVVRPRLHPSF 81

RESULT 7

ID Q865D4 PRELIMINARY; PRT; 145 AA.
 AC Q865D4;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Kappa casein (Fragment)
 DE Ursus arctos (Brown bear) (Grizzly bear)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9644;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=SAK8.1;
 RC Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439924; AAC63799.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR Prodom; PD003689; Casein_kappa.1.
 FT NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16277 MW; B806C09AAB3CB30D CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRAPAIINNPYPRTYANPAVVRPHAOIPROQYLPNSHPPTVVRPRLHPSF 55
 DB 27 YHRPAVPIHQYVPPYAKVAVRPYAOIPQOVLPNAPPTVVRPRLHPSF 81

RESULT 8

ID Q865D3 PRELIMINARY; PRT; 145 AA.
 AC Q865D3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Kappa casein (Fragment)
 DE Ursus arctos (Brown bear) (Grizzly bear)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=9644;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=SAK9.1;
 RC Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439926; AAC63801.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR Prodom; PD003689; Casein_kappa.1.
 FT NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16278 MW; CED59DF7CB3CA0AE CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRAPAIINNPYPRTYANPAVVRPHAOIPROQYLPNSHPPTVVRPRLHPSF 55
 DB 27 YHRPAVPIHQYVPPYAKVAVRPYAOIPQOVLPNAPPTVVRPRLHPSF 81

RESULT 9

ID Q865D2 PRELIMINARY; PRT; 145 AA.
 AC Q865D2;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Kappa casein (Fragment)
 DE Ursus maritimus (Polar bear) (Thalarcos maritimus)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=29073;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=1796.1;
 RC Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 American bears."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439927; AAC63802.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR Prodom; PD003689; Casein_kappa.1.
 FT NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16277 MW; B806C09AAB3CB30D CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRAPAIINNPYPRTYANPAVVRPHAOIPROQYLPNSHPPTVVRPRLHPSF 55
 DB 27 YHRPAVPIHQYVPPYAKVAVRPYAOIPQOVLPNAPPTVVRPRLHPSF 81

```
RESULT 10
Q865D1 PRELIMINARY; PRT; 145 AA.
AC Q865D1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kappa casein (Fragment).
DE Ursus maritimus (Polar bear) (Thalarcos maritimus).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6389.12;
RA Cronin M.A., Nelson R.J., Amstrup S.C., Mickliffe J.;
RT "Variation in the MHC class II DQB and K-casein genes in North
RT American bears.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439931; AAO63804.1; -.
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; Casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 16210 MW; 3538009BAB269A0F CRC64;

Query Match
Best Local Similarity 67.9%; Score 207; DB 6; Length 145;
Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Db 1 YORRPAIANNPVRYTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
27 YPHRPAPVIMHQYVPYPAKPAVVRPYAQIPQOVLPNAVPTVVRHRLHPSF 81

RESULT 11
Q865D0 PRELIMINARY; PRT; 145 AA.
AC Q865D0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kappa casein (Fragment).
DE Ursus maritimus (Polar bear) (Thalarcos maritimus).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6519.4;
RA Cronin M.A., Nelson R.J., Amstrup S.C., Mickliffe J.;
RT "Variation in the MHC class II DQB and K-casein genes in North
RT American bears.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439933; AAO63806.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; Casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 16263 MW; 1817C09AAB3CB30C CRC64;

Query Match
Best Local Similarity 67.9%; Score 207; DB 6; Length 145;
Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Db 1 YORRPAIANNPVRYTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
27 YPHRPAPVIMHQYVPYPAKPAVVRPYAQIPQOVLPNAVPTVVRHRLHPSF 81
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```
RESULT 12
Q861U4 PRELIMINARY; PRT; 145 AA.
AC Q861U4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kappa casein (Fragment).
DE Ursus americanus (American black bear).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9643;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB587.2, NHB2.5, and NHB2.8;
RA Cronin M.A., Nelson R.J., Amstrup S.C., Mickliffe J.;
RT "Variation in the MHC class II DQB and K-casein genes in North
RT American bears.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439901; AAO63784.1; -.
DR EMBL; AF439917; AAO63796.1; -.
DR EMBL; AF439918; AAO63797.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; Casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 16263 MW; 1817C09AAB3CB30C CRC64;

Query Match
Best Local Similarity 67.9%; Score 207; DB 6; Length 145;
Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Db 1 YORRPAIANNPVRYTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
27 YPHRPAPVIMHQYVPYPAKPAVVRPYAQIPQOVLPNAVPTVVRHRLHPSF 81

RESULT 13
Q861U3 PRELIMINARY; PRT; 145 AA.
AC Q861U3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kappa casein (Fragment).
DE Ursus arctos (Brown bear) (Grizzly bear).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GK20.8, and SAK8.7;
RA Cronin M.A., Nelson R.J., Amstrup S.C., Mickliffe J.;
RT "Variation in the MHC class II DQB and K-casein genes in North
RT American bears.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF439905; AAO63788.1; -.
DR EMBL; AF439925; AAO63800.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR000117; Casein_Kappa.
DR Pfam; PF00997; Casein_Kappa; 1.
DR ProDom; PD003689; Casein_Kappa; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 16263 MW; 1817C09AAB3CB30C CRC64;

Query Match
Best Local Similarity 67.9%; Score 207; DB 6; Length 145;
Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
```


QY 1 YORRPAIANNPYPRTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
 Db 27 YPHRPAVPINHQVVPYPAKPAVAVRPAQIPQWQVLPNAVPPVVRPHLHPSF 81

RESULT 14

Q861T9 PRELIMINARY; PRT; 145 AA.
 AC Q861T9;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus arctos (Brown bear) (Grizzly bear).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 OX NCBI_TaxID=9644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GN6.8, and GN7.3;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 RT American bears.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439911; AA063792.1; -.
 DR EMBL; AF439912; AA063793.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR ProDom; PD003689; Casein_kappa.1.
 FT NON_TER 1 1
 FT NON_TER 145 145
 SQ SEQUENCE 145 AA; 16240 MW; 3538109AAB269A0F CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRPAIANNPYPRTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
 Db 27 YPHRPAVPINHQVVPYPAKPAVAVRPAQIPQWQVLPNAVPPVVRPHLHPSF 81

RESULT 15

Q861T8 PRELIMINARY; PRT; 145 AA.
 AC Q861T8;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Kappa casein (Fragment).
 OS Ursus americanus (American black bear).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 OX NCBI_TaxID=9643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB587.8, AB590.9, and MTB2.10;
 RA Cronin M.A., Nelson R.J., Amstrup S.C., Wickliffe J.;
 RT "Variation in the MHC class II DQB and K-casein genes in North
 RT American bears.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF439902; AA063785.1; -.
 DR EMBL; AF439904; AA063787.1; -.
 DR EMBL; AF439913; AA063794.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR InterPro; IPR000117; Casein_kappa.
 DR Pfam; PF00997; casein_kappa.1.
 DR ProDom; PD003689; Casein_kappa.1.
 FT NON_TER 1 1
 FT NON_TER 145 145
 SQ SEQUENCE 145 AA; 16253 MW; 3538109AAB3CB30F CRC64;

Query Match 67.9%; Score 207; DB 6; Length 145;
 Best Local Similarity 67.3%; Pred. No. 7.5e-18;
 Matches 37; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 YORRPAIANNPYPRTYANPAVVRPHAOIPQROYLPNSHPPTVVRPNLHPSF 55
 Db 27 YPHRPAVPINHQVVPYPAKPAVAVRPAQIPQWQVLPNAVPPVVRPHLHPSF 81

Search completed: September 1, 2004, 00:15:33
 Job time : 103.933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:24 ; Search time 115.52 Seconds

(without alignments)
117.402 Million cell updates/sec

Title: US-09-508-095-19

Perfect score: 267

Sequence: 1 GRRRSYQWCAVSGPEATKCF.....VRGPFVSCIKRDSPIQICQA 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	48	2 AAW93883	AAW93883 Bifidobac
2	261	97.8	49	2 AAW93884	AAW93884 Bifidobac
3	261	97.8	51	3 AAB22817	AAB22817 Human lac
4	261	97.8	52	2 AAR87906	AAR87906 Human lac
5	261	97.8	52	2 AAR91192	AAR91192 Lactoferr
6	261	97.8	54	2 AAR88218	AAR88218 Amino aci
7	261	97.8	630	4 AAG77908	AAG77908 Human lac
8	261	97.8	630	4 AAG80724	AAG80724 Codon opt
9	261	97.8	630	5 AAE27884	AAE27884 Human cod
10	261	97.8	632	3 AAY58733	AAY58733 Human lac
11	261	97.8	632	4 AAB97382	AAB97382 Human lac
12	261	97.8	632	4 AAG77906	AAG77906 Human lac
13	261	97.8	632	5 AAR8002	AAR8002 Human cod
14	261	97.8	633	2 AAR85146	AAR85146 Lactoferr
15	261	97.8	705	2 AAR22423	AAR22423 Human lac
16	261	97.8	705	2 AAY31152	AAY31152 Human lac
17	261	97.8	708	2 AAR22424	AAR22424 Human lac
18	261	97.8	708	2 AAY31153	AAY31153 Human lac
19	261	97.8	709	2 AAR45198	AAR45198 Human lac
20	261	97.8	709	2 AAR45199	AAR45199 Human lac
21	261	97.8	711	3 AAW53880	AAW53880 Bovine al
22	261	97.8	711	3 AAY77578	AAY77578 Human lac
23	261	97.8	711	3 AAB03831	AAB03831 Human lac
24	261	97.8	711	4 AAB36843	AAB36843 Human lac
25	261	97.8	711	4 AAG64828	AAG64828 Chronic h

26	261	97.8	711	7 ADE76661	ADE76661 Human lac
27	256	95.9	689	4 AAG77909	AAG77909 Human lac
28	255	95.5	51	3 AAB22824	AAB22824 Lactoferr
29	254	95.1	49	2 AAW93882	AAW93882 Bifidobac
30	254	95.1	51	3 AAB22823	AAB22823 Lactoferr
31	254	95.1	51	3 AAB22822	AAB22822 Lactoferr
32	254	95.1	690	2 AAW71180	AAW71180 Mutant hu
33	254	95.1	709	2 AAW521695	AAW521695 Human lac
34	254	95.1	709	2 AAW53879	AAW53879 Human lac
35	254	95.1	709	3 AAY77577	AAY77577 Human lac
36	254	95.1	709	3 AAB03830	AAB03830 Human lac
37	254	95.1	709	4 AAB36842	AAB36842 Protein e
38	254	95.1	709	7 ADE76659	ADE76659 Human lac
39	254	95.1	711	2 AAR08033	AAR08033 Human lac
40	254	95.1	711	2 AAR43653	AAR43653 Lactoferr
41	254	95.1	711	2 AAW09342	AAW09342 Human lac
42	254	95.1	711	2 AAW57317	AAW57317 Human lac
43	254	95.1	711	2 AAW86021	AAW86021 Human lac
44	254	95.1	711	3 AAB08182	AAB08182 Amino aci
45	254	95.1	711	4 AAB02341	AAB02341 Human lac

ALIGNMENTS

RESULT 1	AAW93883	standard; peptide; 48 AA.
ID	AAW93883	
AC	XX	
XX	AAW93883;	
DT	27-AUG-2003	(revised)
DT	25-JUN-1999	(first entry)
XX		
DE	Bifidobacterium bifidus stimulating peptide 19.	
XX		
KW	Bifidogenic peptide; protease; treatment; microbe-related disease;	
KW	bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;	
KW	infection; inflammation; microbial induced tumour; degenerative disorder;	
KW	diarrhoea; colic; oral microflora; intestinal microflora; caries;	
XX	vaginal microflora.	
OS	Bifidobacterium bifidum.	
XX		
FT	Key	Location/Qualifiers
FT	Disulfide-bond 9..45	
FT	Disulfide-bond 19..36	
XX		
PN	WO9914231-A2.	
PN		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998; 98WO-EP005899.	
XX		
PR	16-SEP-1997; 97DE-01040604.	
PR	11-FEB-1998; 98DE-01005385.	
PA	(FORS/) FORSMANN W.	
XX		
PI	Forsmann W, Zucht H, Liepke C;	
XX		
DR	WPI, 1999-244022/20.	
XX		
PT	Milk-derived peptides that stimulate Bifidobacterium bifidus.	
XX		
PS	Claim 2; Page 3; 25pp; German.	
CC	This invention describes milk-derived bifidogenic peptides and their	
CC	active derivatives or fragments, and combinations of them produced by	
CC	chemical coupling. Such are produced from bovine or human milk by	
CC	treatment for 2 hr with proteases, then centrifuging to remove fat and	
CC	acidifying to pH 2 to precipitate proteins. The solution phase is then	
CC	subjected to reverse-phase high-performance liquid chromatography (HPLC)	

CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
CC Bifidobacterium bifidus and Escherichia coli in presence of the
CC fractions. Those fractions for which (Bw-50)-(Bw-E0) is at least 0.15 are
CC selected where Bw = germ count after 16 hr culture of B. bifidus in 50%
CC Elliker broth containing peptide at 0.2 mg/mL, Bw = germ count under
CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
CC culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2
CC mg/mL. B0 = germ count under similar conditions in a peptide-free
CC control. The peptides AA93865-W93868 are used to treat microbe-related
CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
CC oral, intestinal or vaginal microflora, or caries. (Updated on 27-AUG-
CC 2003 to correct OS field.)

SQ Sequence 48 AA;

Query Match 100.0%; Score 267; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 5.7e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRRSVQWCAVSOPEATKCFQWQRMKRYGPPVSCIKRDSPIQIOA 48
DB 1 GRRSVQWCAVSOPEATKCFQWQRMKRYGPPVSCIKRDSPIQIOA 48

RESULT 2

ID AA93864 standard; peptide; 49 AA.

AC AA93864;

DT 27-AUG-2003 (revised)
DT 25-JUN-1999 (first entry)

DE Bifidobacterium bifidus stimulating peptide 20.

KW Bifidogenic peptide; protease; treatment; microbe-related disease;
KW Bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
KW infection; inflammation; microbial induced tumour; degenerative disorder;
KW diarrhoea; colic; oral microflora; intestinal microflora; caries;
KW vaginal microflora.

OS Bifidobacterium bifidum.

FH Key Location/Qualifiers

FT Disulfide-bond 10. 46
FT Disulfide-bond 20. 37

PN WO914231-A2.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-EP005899.

PR 16-SEP-1997; 97DE-01040604.

PR 11-FEB-1998; 98DE-01005385.

PA (FORS/) FORSSMANN W.

PI Forssmann W, Zucht H, Liepke C;

DR WPI; 1999-244022/20.

PT Milk-derived peptides that stimulate Bifidobacterium bifidus.

PS Claim 2; Page 3; 25pp; German.

CC This invention describes milk-derived bifidogenic peptides and their
CC active derivatives or fragments, and combinations of them produced by
CC chemical coupling. Such are produced from bovine or human milk by
CC treatment for 2 hr with proteases, then centrifuging to remove fat and

CC acidifying to pH 2 to precipitate proteins. The solution phase is then
CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
CC Bifidobacterium bifidus and Escherichia coli in presence of the
CC fractions. Those fractions for which (Bw-50)-(Bw-E0) is at least 0.15 are
CC selected where Bw = germ count after 16 hr culture of B. bifidus in 50%
CC Elliker broth containing peptide at 0.2 mg/mL, Bw = germ count under
CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
CC culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2
CC mg/mL. B0 = germ count under similar conditions in a peptide-free
CC control. The peptides AA93865-W93868 are used to treat microbe-related
CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
CC oral, intestinal or vaginal microflora, or caries. (Updated on 27-AUG-
CC 2003 to correct OS field.)

SQ Sequence 49 AA;

Query Match 97.8%; Score 261; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRRSVQWCAVSOPEATKCFQWQRMKRYGPPVSCIKRDSPIQIOA 48
DB 3 RRRSVQWCAVSOPEATKCFQWQRMKRYGPPVSCIKRDSPIQIOA 49

RESULT 3

ID AAB22817 standard; protein; 51 AA.

AC AAB22817;

DT 03-JAN-2001 (first entry)

DE Human lactoferrin fragment, SEQ ID NO:2.

KW Human lactoferrin fragment; host-defence peptide; antimicrobial;
KW endotoxin neutralisation; Gram negative bacterium; lipopolysaccharide;
KW LPS; antibacterial; antifungal; sepsis; septic shock; tuberculosis;
KW leprosy.

OS Homo sapiens.

FN WO200049040-A2.

PD 24-AUG-2000.

PF 27-JAN-2000; 2000WO-IB000271.

PR 05-FEB-1999; 99US-00245527.

PA (ENDO-) ENDOGEN RES PH AB.

PI Mann DM;

DR WPI; 2000-558291/51.

CC Antimicrobial/endotoxin neutralizing polypeptide generated by proteolytic
CC digestion of lactoferrin, useful for treatment of bacterial and fungal
CC infections, and for preventing contamination of e.g. food products,
CC living cells, and blood.

PS Claim 5; Page 8; 90pp; English.

CC The invention relates to proteolytic fragments of lactoferrin (Lf) and
CC variants thereof which act as host-defence peptides, having antimicrobial
CC and endotoxin-neutralising activity. The peptides are useful for
CC treatment of bacterial and fungal infections, and may be particularly
CC used for treating sepsis, tuberculosis and leprosy. The peptides are also
CC useful for treating a variety of products at risk of contamination with

CC microorganisms and endotoxin (lipopolysaccharide, LPS), such as food
 CC products, tissue, living cells, blood, drugs, glassware and surgical
 CC equipment. Sequences AAB22817 and AAB22822-B22827 represent specifically
 CC claimed human lactoferrin-derived polypeptides of the invention. The
 CC present sequence is a 6 kD fragment of human lactoferrin comprising the N
 CC -terminal 51 residues produced via cathepsin D digestion
 XX

SO Sequence 51 AA;

Query Match 97.8%; Score 261; DB 3; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.1e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 48
 DB 3 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 49

RESULT 4
 AAB87906
 ID AAB87906 standard; peptide; 52 AA.

AC AAB87906;
 DT 01-MAR-1996 (first entry)
 XX
 DE Human lactoferrin (1-52).
 XX
 KM antiviral; lactoferrin.
 XX
 OS Synthetic.

XX
 FT Key Location/Qualifiers
 FT Disulfide-bond 10..46 /note="each Cys residue may be in reduced form or may
 FT form a disulfide bond with another Cys residue. A 10-46
 FT disulfide bond is exemplified"
 FT 20..37
 FT /note="each Cys residue may be in reduced form or may
 FT form a disulfide bond with another Cys residue. A 20-37
 FT disulfide bond is exemplified"

XX JP07069915-A.
 XX 14-MAR-1995.
 XX
 PD 02-SEP-1993; 93JP-00240284.
 XX
 PR 02-SEP-1993; 93JP-00240284.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1995-144726/19.

PT Inhibitor against viral infection and proliferation - contains peptide
 PT having sequence from lactoferrin.

XX Claim 2; Page 2; 10pp; Japanese.

XX The sequence is one of six peptides disclosed as having inhibitory effect
 CC against viral infection. The peptides are derived from lactoferrin. Their
 CC activity is demonstrated against cytomegalovirus
 XX

SO Sequence 52 AA;

Query Match 97.8%; Score 261; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.2e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 48
 DB 3 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 49

RESULT 5
 AAB91192
 ID AAB91192 standard; peptide; 52 AA.

XX AAB91192;

DT 06-SEP-1996 (first entry)

DE Lactoferrin decomposition peptide.

KW immunosuppressor; antiviral; cytomegalovirus; cosmetic; food; feed;
 KW lymphocyte blastogenesis.

OS Synthetic.

XX
 FT Key Location/Qualifiers
 FT Disulfide-bond 10..46 /note="optionally this bond may be reduced"
 FT 20..37 /note="optionally this bond may be reduced"

XX JP08073499-A.
 XX 19-MAR-1996.

PF 01-SEP-1994; 94JP-00232026.

PR 01-SEP-1994; 94JP-00232026.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1996-205535/21.

PT New peptide(s) derived from human lactoferrin - are useful as
 PT immunosuppressors, esp. for preventing infection by cytomegalovirus.

XX Claim 3; Page 2; 11pp; Japanese.

XX The present sequence is one of four new peptides (see AAB91191 -
 CC AAB91193) obtained by enzymatically decomposing lactoferrin using
 CC protease. The peptides are immunosuppressors which induce blastogenesis of
 CC lymphocytes and are particularly useful for treating cytomegalovirus
 CC infection. They can be used in drugs and cosmetics and can be added to
 CC foods and feeds
 XX

SO Sequence 52 AA;

Query Match 97.8%; Score 261; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.2e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 48
 DB 3 RRRSVQWCAVSQPEATKCFQWQNRKRVGPPVSCIRKDSPIQICQA 49

RESULT 6
 AAB88218

ID AAB88218 standard; peptide; 54 AA.

XX AAB88218;

DT 12-JUN-1996 (first entry)

DE Amino acid sequence contg. lactoferrin antibacterial peptide.

XX Recombinant vector; human; lactoferrin; antibacterial peptide;
 KW regulatory sequence; tac; promoter; shuttle; vector; pGEX2; GAD1; pGEM2;
 KW Rous Sarcoma Virus; long terminal repeat; pRSVcat; lactoferrin.
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 19..29
 /note="lactoferrisin antibacterial peptide"
 XX JPC07274970-A.
 XX 24-OCT-1995.
 XX 01-APR-1994; 94UP-00085244.
 PF 01-APR-1994; 94UP-00085244.
 PR 01-APR-1994; 94UP-00085244.
 XX (MORG) MORINAGA MILK IND CO LTD.
 PA WPI; 1995-399338/51.
 DR
 XX Recombinant vector contg. lactoferrisin gene - used to prepare an
 PT antibacterial peptide.
 PS Claim 7; Page 11; 18pp; Japanese.
 CC A recombinant vector in which a DNA sequence encoding at least the
 CC genetic lactoferrisin antibacterial peptide AAR88216 (specific examples
 CC of which are given in AAR84083-85) is inserted, pref. downstream of the
 CC vector's regulatory sequence, is claimed. Pref. examples of amino acid
 CC sequences contg. the above peptide are given in AAR88217/18. The
 CC regulatory sequence is the tac promoter from shuttle vector pGEX2, the
 CC GalI promoter from vector pXOM2 or Rous Sarcoma Virus long terminal
 CC repeat from vector pRSVNOT
 CC
 SQ Sequence 54 AA;
 Query Match 97.8%; Score 261; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 4.3e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RRRSVQWCAVSQPEATKCFQWRNMRKVRGPPVSCIIRDSPIQICIA 48
 DB 3 RRRSVQWCAVSQPEATKCFQWRNMRKVRGPPVSCIIRDSPIQICIA 49
 RESULT 7
 AAG77908
 ID AAG77908 standard; protein; 690 AA.
 AC AAG77908;
 XX 22-JAN-2002 (first entry)
 DE Human lactoferrin variant hLF-2N.
 DE
 KW Human; lactoferrin; hLF; infectious disease; inflammatory disease;
 KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
 KW anaemia; myelopolesis; reperfusion injury; cytokine release;
 KW proteoglycan; hLF-2N; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 26..29
 /label=Cationic_domain
 XX WO200172322-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-NI000253.
 PF 27-MAR-2000; 2000EP-00201110.
 PR 27-MAR-2000; 2000US-0193352P.
 XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
 XX

PI Van Bree JBMW, Nuijens JH;
 XX WPI; 2001-648424/74.
 DR
 XX Use of lactoferrin for treatment of infectious diseases, inflammatory
 PT diseases and excess of heparin.
 PS Claim 10; Page; 49pp; English.
 CC The sequence represents the human lactoferrin (hLF) protein variant hLF-
 CC 2N. The invention relates to novel methods of treatment using high doses
 CC of lactoferrin. The methods of the invention are useful for the treatment
 CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis, and
 CC anaemia, myelopolesis, reducing reperfusion injury, cytokine release and
 CC proteoglycan-mediated entry of virus into cells. The advantage of the
 CC method is that the patient is substantially free of side effect responses
 CC to administration of lactoferrin. Therefore large doses of lactoferrin
 CC can be administered. Note: The present sequence is not shown in the
 CC specification but is derived from human wild-type lactoferrin sequence
 CC given in the sequence listing of the specification
 CC
 SQ Sequence 690 AA;
 Query Match 97.8%; Score 261; DB 4; Length 690;
 Best Local Similarity 100.0%; Pred. No. 7.9e-27;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RRRSVQWCAVSQPEATKCFQWRNMRKVRGPPVSCIIRDSPIQICIA 48
 DB 1 RRRSVQWCAVSQPEATKCFQWRNMRKVRGPPVSCIIRDSPIQICIA 47
 RESULT 8
 ABG80724
 ID ABG80724 standard; protein; 690 AA.
 AC ABG80724;
 XX 29-NOV-2002 (first entry)
 DE Codon optimised lactoferrin protein.
 DE
 KW Transformed plant; heterologous transcription factor; transgenic plant;
 KW seed protein; protein expression.
 XX
 OS Homo sapiens.
 XX
 PN WO200264750-A2.
 XX 22-AUG-2002.
 PD 14-FEB-2002; 2002WO-US004909.
 PF 14-FEB-2001; 2001US-0269188P.
 PR 14-FEB-2001; 2001US-0269199P.
 PR 02-MAY-2001; 2001US-00847232.
 XX (VENT-) VENTRIA BIOSCIENCE.
 PA
 XX Huang N, Yang D;
 PI WPI; 2002-657592/70.
 DR N-PSDB; ABS66515.
 XX Producing heterologous polypeptide in plant grain, by culturing
 PT transformed plant to form a grain-producing transforming plant, and
 PT recovering transgenic grains containing polypeptide from transformed
 PT plant.
 XX Examepe 15; Page 117; 230pp; English;
 PS The invention describes a method of producing a heterologous polypeptide
 CC

CC (1) in a grain of a plant, comprising culturing a transformed plant (P1)
CC comprising a first chimeric gene, and optionally, at least one
CC heterologous transcription factor that is capable of enhancing the
CC expression of the chimeric gene, to form a grain producing transforming
CC plant (P2), and recovering transgenic grains containing (1) from P2. The
CC method is useful for producing heterologous polypeptide in a grain of a
CC plant. (1) is a non-plant storage, human or non-human animal, milk or
CC other than a milk polypeptide, antibodies, cytokines, lymphokines,
CC chemokines, hormones, growth factors, coagulation factors, anti-
CC infectives, or cytotoxins, or anti-inflammatory molecule or intestinal
CC trefoil factor (ITF) or its active fragment. Preferably, (1) is
CC lactoferrin, lysozyme, lactoferricin, ITF, epidermal growth factor (EGF),
CC keratinocyte growth factor (KGF), insulin-like growth factor I (IGF-1),
CC lactoferrin, kappa-casein, haptocorrin, lactoperoxidase, alpha-1-
CC antitrypsin, immunoglobulin, alpha-lactalbumin, beta-lactoglobulin,
CC alpha-casein, beta-casein, albumin, fibrinogen or protease inhibitor.
CC This is the amino acid sequence of a protein associated with method of
CC producing a transgenic plant

XX Sequence 690 AA;

Query Match 97.8%; Score 261; DB 5; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.9e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48
DB 3 RRSVQWCAVSQPEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 49

RESULT 9

ID AAE27884 standard; protein; 690 AA.

AC AAE27884;

DT 27-DEC-2002 (first entry)

XX Human codon optimised lactoferrin.

XX Human; feed improvement; plant-derived feed; antibiotic; additive;
XX anti-microbial; poultry; lactoferrin; flour; malt.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

XX Misc-difference 319..320

XX /note="Encoded by CTG TAC CTC"

XX WO200263975-A2.

XX 22-AUG-2002.

XX 14-FEB-2002; 2002WO-US004919.

XX 14-FEB-2001; 2001US-0269188P.

XX 02-MAY-2001; 2001US-00847232.

XX (VENT-) VENTRIA BIOSCIENCE.

XX Huang N, Rodriguez RL, Hagie FE;

XX WPI; 2002-682708/73.

XX N-PSDB; AAD45297.

XX Improved feed for production animals, comprising plant-derived feed
XX ingredients, and seed composition containing flour, extract, or malt from
XX mature monocot seeds and heterologous seed-produced anti-microbial
XX proteins.

XX Example 7; Page 148-150; 175pp; English.

CC The invention relates to improved feed for production animals, comprising
CC one or more plant-derived feed ingredients, substantially unsupplemented
CC with small-molecule antibiotics and as an additive a seed composition
CC containing a flour, extract or malt obtained from mature monocot seeds
CC and one or more heterologous seed-produced anti-microbial proteins in
CC substantially unpurified form. The invention is useful as a feed for
CC production animals such as poultry and hocked farm animals. The present
CC sequence is human codon optimised lactoferrin. This sequence is used in
CC the invention

XX Sequence 690 AA;

Query Match 97.8%; Score 261; DB 5; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.9e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48
DB 3 RRSVQWCAVSQPEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 49

RESULT 10

ID AAY58733 standard; protein; 692 AA.

AC AAY58733;

DT 25-APR-2000 (first entry)

XX Human lactoferrin.

XX Lactoferrin; human; transgenic plant.

XX Homo sapiens.

XX WO200004146-A1.

XX 27-JAN-2000.

XX 19-JUL-1999; 99WO-IT000226.

XX 17-JUL-1999; 98IT-RM000478.

XX (PLAN-) PLANTECHNO SRL.

XX Fogher C;

XX WPI; 2000-161129/14.

XX N-PSDB; AAY58122.

XX Synthetic polynucleotide encoding human lactoferrin, used for production
XX of functional foods, vegetal milks and human lactoferrin.

XX Disclosure: Page 73-77; 93pp; English.

XX The present sequence is that of human lactoferrin. The invention relates
XX to a synthetic gene (see AAY58122) that encodes human lactoferrin but
XX which has codon usage designed to maximise expression in plants.
XX Transgenic plants that express human lactoferrin in a tissue-specific
XX manner, especially in the seeds, can be used in processes for the
XX production of functional vegetal milk, fruit juices, fruit and/or
XX vegetable homogenized foods (claimed). The transgenic plants are selected
XX from solanaceae, cereals, leguminosae, fruit bearing plants and
XX horticultural plants, especially soybean, tobacco and rice

XX Sequence 692 AA;

Query Match 97.8%; Score 261; DB 3; Length 692;
Best Local Similarity 100.0%; Pred. No. 7.9e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48

Db 3 RRSVOMCAVSOPEATKCFOWQRMKRVGPPVSCIKRDSPIQICIA 49

RESULT 11

ID AAB97382 standard; protein; 692 AA.

XX AAB97382;

XX AC AAB97382;

XX DT 17-AUG-2001 (first entry)

XX DE Human lactoferrin (hLF).

XX DE Human lactoferrin (hLF).

XX KW Human; lactoferrin; hLF; N-terminal; antimicrobial; heparin;

XX KW inflammatory response; cytokine production reduction;

XX KW neutrophil degranulation; myelopoiesis inhibition.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Region 1..27 /note="Fragments of the N-terminal are specifically

FT Domain 2..5 /label= Cationic_domain

FT Domain 28..31 /label= Cationic_domain

FT Domain /label= Cationic_domain

XX PN WO200134641-A2.

XX PD 17-MAY-2001.

XX PF 10-NOV-2000; 2000MO-NL000621.

XX PR 11-NOV-1999; 99EP-00203775.

XX PR 11-NOV-1999; 99US-0164975P.

XX PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.

XX PI Van Berkel PHC, Nibbering PH, Nuijens JH;

XX DR WPI; 2001-335909/35.

XX PT New polypeptides comprising the N-terminal region of human lactoferrin

XX PT protein exhibit higher antimicrobial activity than the full length

XX PT protein and are useful to treat bacterial infections.

XX PS Claim 1; Page 55-57; 59pp; English.

XX CC This invention relates to fragments (between 6 and 26 amino acids) of the

XX CC human lactoferrin hLF protein (represented by the present sequence). N-

XX CC terminal hLF peptides have antimicrobial activity. The peptides of the

XX CC invention are used to treat microbial infections, especially infections

XX CC by gram positive or negative bacteria, particularly *Listeria*, *Staphylococcus*, *Klebsiella* or *Escherichia* species, especially *L.*

XX CC *monocytogenes*, *S. aureus* and *E. coli*. Other uses include reducing

XX CC inflammatory response by neutralising heparin or lipopolysaccharide or by

XX CC reducing cytokine production and neutrophil degranulation, inhibiting

XX CC entry of viruses such as cytomegalovirus, herpes simplex virus 1 or HIV

XX CC into cells, inhibiting myelopoiesis and reducing production of GM-CSF

XX CC (granulocyte/macrophage colony stimulating factor)

XX SQ Sequence 692 AA;

Query Match 97.8%; Score 261; DB 4; Length 692;

Best Local Similarity 100.0%; Pred. No. 7.9e-27;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRSVOMCAVSOPEATKCFOWQRMKRVGPPVSCIKRDSPIQICIA 48

DB 3 RRSVOMCAVSOPEATKCFOWQRMKRVGPPVSCIKRDSPIQICIA 49

RESULT 12

ID AAG77906

XX AAG77906 standard; protein; 692 AA.

XX AC AAG77906;

XX DT 18-JAN-2002 (first entry)

XX DE Human lactoferrin.

XX DE Human lactoferrin.

XX KW Human; lactoferrin; hLF; infectious disease; inflammatory disease;

XX KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;

XX KW anaemia; myelopoiesis; reperfusion injury; cytokine release;

XX KW proteoglycan.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Region 2..5 /label= Cationic_domain

FT Domain 28..31 /label= Cationic_domain

FT Domain /label= Cationic_domain

XX PN WO200172342-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-NL000253.

XX PR 27-MAR-2000; 2000EP-00201110.

XX PR 27-MAR-2000; 2000US-0193352P.

XX PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.

XX PI Van Bree JBM, Nuijens JH;

XX DR WPI; 2001-648424/74.

XX PT Use of lactoferrin for treatment of infectious diseases, inflammatory

XX PT diseases and excess of heparin.

XX PS Claim 26; Page 47-49; 49pp; English.

XX CC The sequence represents the human lactoferrin (hLF) protein. The methods

XX CC of the invention are useful for the treatment or prophylaxis of

XX CC infectious diseases, inflammatory diseases and excess of heparin e.g.

XX CC gastroenteritis, inflammatory bowel disease, sepsis, anaemia, and

XX CC myelopoiesis, reducing reperfusion injury, cytokine release and

XX CC proteoglycan-mediated entry of virus into cells. The advantage of the

XX CC method is that the patient is substantially free of side effect responses

XX CC to administration of lactoferrin. Therefore large doses of lactoferrin

XX CC can be administered

XX SQ Sequence 692 AA;

Query Match 97.8%; Score 261; DB 4; Length 692;

Best Local Similarity 100.0%; Pred. No. 7.9e-27;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRSVOMCAVSOPEATKCFOWQRMKRVGPPVSCIKRDSPIQICIA 48

DB 3 RRSVOMCAVSOPEATKCFOWQRMKRVGPPVSCIKRDSPIQICIA 49

RESULT 13

ID AAE28002

XX AAE28002 standard; protein; 692 AA.

XX AC AAE28002;

XX DT 13-DEC-2002 (first entry)

XX DE Human codon optimised lactoferrin.


```

XX Human; plant-derived food; flour; malt; monocoat seed; milk protein;
KW infant formula; lactoferrin.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 320..321
FT /note="These amino acid residues are absent in the
FT sequence shown as SEQ ID NO:2 in sequence listing of the
FT specification"
XX WO200264814-A2.
XX 22-AUG-2002.
XX
XX 14-FEB-2002; 2002WO-US004921.
XX
XX 14-FEB-2001; 2001US-0269199P.
XX
XX 02-MAY-2001; 2001US-00847232.
XX
XX (VENT-) VENTRIA BIOSCIENCE.
XX
XX Huang N, Rodriguez RL, Hagie FE;
XX
XX WPI; 2002-667011/71.
XX
XX N-PSDB; AAD44922.
XX
XX New nutritionally enhanced food compositions, useful for improving infant
XX formula, or supplementing or enhancing the diet of infants, particularly
XX very-low birth weight infants.
XX
XX Example 9; Page 104; 179pp; English.
XX
XX The invention relates to a nutritionally enhanced food comprising one or
XX more plant-derived food ingredients, and as an additive, a seed
XX composition containing a flour, extract, or malt obtained from mature
XX monocoat seeds and one or more seed-produced human milk proteins in
XX substantially unpurified form. The nutritionally enhanced food and food
XX additive compositions are useful for improving infant formula. Infant
XX formulae containing the recombinant human milk proteins are useful in
XX supplementing or enhancing the diet of infants, particularly very-low
XX birth weight infants. The present sequence is human codon optimised
XX lactoferrin
XX
XX Sequence 692 AA;
XX
XX Query Match 97.8%; Score 261; DB 5; Length 692;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-27;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 RRRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 48
XX |||
XX 3 RRRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 49
XX |||
XX
XX RESULT 14
XX AAR85146
XX ID AAR85146 standard; protein; 693 AA.
XX
XX AAR85146;
XX
XX 02-FEB-1996 (first entry)
XX
XX Lactoferrin protein.
XX
XX Lactoferrin; antiseptic; dietary supplement; iron sequestration;
XX Pichia pastoris.
XX
XX Homo sapiens.
XX
XX WO9530339-A1.
XX

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```

PD 16-NOV-1995.
XX
XX 05-MAY-1995; 95WO-US005653.
XX
XX 05-MAY-1994; 94US-00238445.
XX
XX (FER-) FERRODYNAMICS INC.
XX
XX Kruzel ML, Kurecki T, Gollnick P, Doyle D;
XX
XX WPI, 1995-403891/51.
XX
XX N-PSDB; AAT02999.
XX
XX New isolated DNA encoding human lactoferrin protein - useful for
XX inhibiting microbial growth and iron deficiency, and for sequestering
XX iron or retarding food spoilage.
XX
XX Disclosure; Fig 3a-d; 43pp; English.
XX
XX cDNA encoding human lactoferrin (AAR85146) was isolated from a human
XX mammary gland library and inserted into vector pUC118. Expression in
XX Pichia pastoris GTS 115 (His4) allowed the prodn. of large amounts of the
XX lactoferrin protein, useful as an antiseptic, dietary supplement, etc
XX
XX Sequence 693 AA;
XX
XX Query Match 97.8%; Score 261; DB 2; Length 693;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-27;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 RRRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 48
XX |||
XX 4 RRRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 50
XX |||
XX
XX RESULT 15
XX AAR22423
XX ID AAR22423 standard; protein; 705 AA.
XX
XX AAR22423;
XX
XX 25-MAR-2003 (revised)
XX
XX 17-DEC-2001 (revised)
XX
XX 05-AUG-1992 (first entry)
XX
XX Human lactoferrin deduced from clone HLF 1212.
XX
XX anti-bacterial; anti-viral; anti-fungal; Colony stimulating factor; CSF;
XX release; leukaemia; breast cancer; hormonal regulation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 22
FT /note="Insertion, c.f. B.F.Anderson et al, 1989"
FT
FT Misc-difference 31
FT /note="Substitution, c.f. B.F.Anderson et al, 1989"
FT
FT Misc-difference 55
FT /note="Substitution, c.f. B.F.Anderson et al, 1989"
FT
FT Misc-difference 218
FT /note="Substitution, c.f. B.F.Anderson et al, 1989"
XX
XX USN707502-N.
XX
XX 18-FEB-1992.
XX
XX 31-MAY-1991; 91US-00707502.
XX
XX 31-MAY-1991; 91US-00707502.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
XX Teng C, Pamela TJ;
XX

```

XX MFI, 1992-113934/14.
DR N-PSDB; AAQ23453.
XX
PT Human lactoferrin gene and promoter - used for producing protein for
PT treating e.g. AIDS, neutropenia, skin infections, vaginal infections or
PT septic shock.
XX
PS Example 2; Fig 10; 55pp; English.
XX
CC A Cloneteck cDNA library from normal human breast tissue (HL1037b) was
CC plated in host cells 71090, filter-lifted and probed with mouse
CC lactoferrin cDNA T267. Positive clones were plaque-purified and the
CC inserts subcloned into the EcoRI site of Bluescript II SK+. The
CC recombinant clones were transformed into XLI Blue cells. The longest
CC insert (HLF 1212) was sequenced and was 2117bp in length. The amino acid
CC sequence coded for by HLF 1212 has 4 sites that differ from the
CC previously published revised amino acid sequence derived from the protein
CC (B.F. Anderson et al., J.Mol.Biol. 209: 711-734, 1989). Also contained
CC within HLF 1212, but not in any of the other partially sequenced
CC isolates, is a deleted cytosine at bp 2097 (AA 699) which caused a
CC frameshift at the 3' end of the coding sequence. The deletion is thought
CC to be either a cloning artefact or a rare species of mRNA. See also
CC AAQ23454 and AAQ23455. (Note: Revised entry submitted to correct the
CC patent number format of US Government-owned NTIS applications to prevent
CC clashes with ongoing US granted patent numbers. For further information
CC please visit the Derwent web site at
CC www.derwent.com/dwpi/updates/ntis.html.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 705 AA;

Query Match 97.8%; Score 261; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 8.1e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQCAVSOPEATKCFQWQNNRKYRGPPVSCIKRDSPIQCTQA 48
|||
DB 20 RRRSVQCAVSOPEATKCFQWQNNRKYRGPPVSCIKRDSPIQCTQA 66

Search completed: September 1, 2004, 00:03:49
Job time : 115.52 secs

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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:04:10 ; Search time 31.04 Seconds
(without alignments)
79,834 Million cell updates/sec

Title: US-09-508-095-19

Perfect score: 267
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCBUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	97.8	54	2	US-08-464-182A-2
2	261	97.8	54	2	US-08-406-271-2
3	261	97.8	694	3	US-08-724-586-2
4	261	97.8	694	4	US-09-421-632-2
5	261	97.8	694	4	US-09-932-190-2
6	261	97.8	705	2	US-08-655-640-2
7	261	97.8	708	2	US-08-655-640-4
8	261	97.8	711	1	US-08-154-019-4
9	261	97.8	711	3	US-08-461-333-4
10	261	97.8	711	3	US-08-464-167-4
11	261	97.8	711	3	US-09-158-313-4
12	261	97.8	711	3	US-08-476-798-4
13	260	97.4	53	2	US-08-464-182A-5
14	260	97.4	53	2	US-08-406-271-5
15	264	95.1	52	4	US-09-017-043A-3
16	254	95.1	709	1	US-08-154-019-2
17	254	95.1	709	1	US-08-461-333-2
18	254	95.1	709	3	US-08-464-167-2
19	254	95.1	709	3	US-09-158-313-2
20	254	95.1	709	3	US-08-476-798-2
21	254	95.1	711	1	US-08-145-681-2
22	254	95.1	711	1	US-08-250-308-2
23	254	95.1	711	1	US-08-453-703-2
24	254	95.1	711	2	US-08-456-106-2
25	254	95.1	711	3	US-08-456-108-2
26	254	95.1	711	3	US-09-265-577-2
27	254	95.1	711	4	US-09-633-739-2

28	254	95.1	711	5	PCT-US93-03614-2	Sequence 2, Appl
29	252	94.4	47	2	US-08-464-182A-6	Sequence 6, Appl
30	252	94.4	47	2	US-08-406-271-6	Sequence 6, Appl
31	250	93.6	50	2	US-08-693-274A-7	Sequence 7, Appl
32	200	74.9	36	1	US-07-755-161A-8	Sequence 8, Appl
33	200	74.9	36	1	US-07-891-174-8	Sequence 8, Appl
34	200	74.9	36	1	US-08-256-771-30	Sequence 30, Appl
35	200	74.9	36	1	US-08-381-984-29	Sequence 29, Appl
36	159	59.6	48	2	US-08-693-274A-10	Sequence 10, Appl
37	159	59.6	50	4	US-09-017-043A-5	Sequence 5, Appl
38	159	59.6	52	2	US-08-464-182A-17	Sequence 17, Appl
39	159	59.6	52	2	US-08-406-271-17	Sequence 17, Appl
40	142	53.2	25	1	US-07-755-161A-10	Sequence 10, Appl
41	142	53.2	25	1	US-07-891-174-10	Sequence 10, Appl
42	142	53.2	25	1	US-08-204-487-7	Sequence 7, Appl
43	141	52.8	30	2	US-08-464-182A-4	Sequence 4, Appl
44	141	52.8	30	2	US-08-406-271-4	Sequence 4, Appl
45	134	50.2	51	4	US-09-017-043A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-464-182A-2
Sequence 2, Application US/08464182A
Patent No. 5849885
GENERAL INFORMATION:
APPLICANT: Nuijens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: Isolation of Lactoferrin from Milk
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,182A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,271
FILING DATE: 09-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-004920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..54
OTHER INFORMATION: /note= "HLF CDNA of GPF"

US-08-464-182A-2

Query Match 97.8%; Score 261; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 48
DB 3 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 49

RESULT 2

US-08-406-271-2
Sequence 2, Application US/08406271
Patent No. 5919913

GENERAL INFORMATION:

APPLICANT: Nyvens, Jan H.

APPLICANT: Van Veen, Harry H.

TITLE OF INVENTION: Isolation of Lactoferrin from Milk

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: TOWNSEND and CREW LLP

STREET: One Market Plaza, Stewart Street Tower, 20th

CITY: San Francisco

STATE: CA USA

COUNTRY: CA USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,271

FILING DATE: 09-MAR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/198,321

FILING DATE: 16-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 016994-004910

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURES:

NAME/KEY: Peptide

LOCATION: 1..54

OTHER INFORMATION: /note= "HLF CDNA of GPE"

US-08-406-271-2

Query Match 97.8%; Score 261; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 48
DB 3 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 49

RESULT 3

US-08-724-586-2

Sequence 2, Application US/08724586

Patent No. 6066469

GENERAL INFORMATION:

APPLICANT: Krusel, Marian L.

APPLICANT: Kurecki, Tomasz

APPLICANT: Gollnick, Paul D.

APPLICANT: Doyle, Darrell J.

TITLE OF INVENTION: Cloning, Expression, and Uses of Human

Lactoferrin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Jacobson, Price, Holman & Stern

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,586

FILING DATE: 30-SEPT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/238,445

FILING DATE: 05-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10505/P58185C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666

TELEFAX: (202) 393-5350

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 694 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-724-586-2

Query Match 97.8%; Score 261; DB 3; Length 694;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 48
DB 5 RRSVQWCAVSQPEATKCFQWQNNRKXVGPVSCIKRDSPIQICIA 51

RESULT 4

US-09-421-632-2

Sequence 2, Application US/09421632

Patent No. 6277817

GENERAL INFORMATION:

APPLICANT: Krusel, Marian L.

APPLICANT: Kurecki, Tomasz

APPLICANT: Gollnick, Paul D.

APPLICANT: Doyle, Darrell J.

TITLE OF INVENTION: Cloning, Expression, and Uses of Human

Lactoferrin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Jacobson, Price, Holman & Stern

STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,586
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-421-632-2

Query Match
Best Local Similarity 97.8%; Score 261; DB 3; Length 694;
Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
2 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 48
5 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 51

RESULT 5
US-09-932-190-2
Sequence 2, Application US/09932190
Patent No. 6455687
GENERAL INFORMATION:
APPLICANT: Krusel, Marian L.
Krusel, Tomasz
Golnick, Paul D.
Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/932,190
FILING DATE: 17-AUG-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-932-190-2

Query Match
Best Local Similarity 97.8%; Score 261; DB 4; Length 694;
Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
2 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 48
5 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 51

RESULT 6
US-08-655-640-2
Sequence 2, Application US/08655640
Patent No. 5948613
GENERAL INFORMATION:
APPLICANT: Teng, Christina
Panella, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-640-2

Query Match
Best Local Similarity 97.8%; Score 261; DB 2; Length 705;
Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
2 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 48
5 RRSVQWCAVSOPEATKCFQWQRMKRVGPPVSCIKRDSPIQIA 66

RESULT 7
US-08-655-640-4
Sequence 4, Application US/08655640
Patent No. 5948613
GENERAL INFORMATION:

```

APPLICANT: Teng, Christina
APPLICANT: Panella, Timothy J.
TITLE OF INVENTION: HUMAN LACTOFERRIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARRY & CUSHMAN
STREET: 1100 NEW YORK AVE. N.W., NINTH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,640
FILING DATE: 30-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,538
FILING DATE: December 17, 1992
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5663/98019/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-640-4

Query Match 97.8%; Score 261; DB 2; Length 708;
Best Local Similarity 100.0%; Pred. No. 2e-27; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0

Cy 2 RRSVQWCAVSQPEATKCFQWQRMNRKVRGPVSCIKRDSPIQICQA 48
Db 22 RRSVQWCAVSQPEATKCFQWQRMNRKVRGPVSCIKRDSPIQICQA 68

RESULT 8
US-08-154-019-4
Sequence 4, Application US/08154019
Patent No. 5633076
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,019
FILING DATE: 16-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheut, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-154-019-4

Query Match 97.8%; Score 261; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-27; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0

Cy 2 RRSVQWCAVSQPEATKCFQWQRMNRKVRGPVSCIKRDSPIQICQA 48
Db 22 RRSVQWCAVSQPEATKCFQWQRMNRKVRGPVSCIKRDSPIQICQA 68

RESULT 9
US-08-461-333-4
Sequence 4, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333

FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-333-4

Query Match 97.8%; Score 261; DB 1; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSOPEATKCFQWQRMKXRGPPVSCIKRDSPIQICQ 48
DB 22 RRSVQWCAVSOPEATKCFQWQRMKXRGPPVSCIKRDSPIQICQ 68

RESULT 10
US-08-464-167-4
Sequence 4, Application US/08464167
Patent No. 6013857
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-167-4

Query Match 97.8%; Score 261; DB 3; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSOPEATKCFQWQRMKXRGPPVSCIKRDSPIQICQ 48
DB 22 RRSVQWCAVSOPEATKCFQWQRMKXRGPPVSCIKRDSPIQICQ 68

RESULT 11
US-09-158-313-4
Sequence 4, Application US/09158313
Patent No. 6066725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-313-4

Query Match 97.8%; Score 261; DB 3; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQIOA 68

RESULT 12
US-08-476-798-4
Sequence 4, Application US/08476798
Patent No. 6140552
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert J.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschultz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-798-4

Query Match 97.8%; Score 261; DB 3; Length 711;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQIOA 68

RESULT 13
US-08-464-182A-5
Sequence 5, Application US/08464182A
Patent No. 5849885
GENERAL INFORMATION:
APPLICANT: Nuijens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: Isolation of Lactoferrin from Milk
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,182A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,271
FILING DATE: 09-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-004920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..53
OTHER INFORMATION: /note= "HLF CDNA Rado"
US-08-464-182A-5

Query Match 97.4%; Score 260; DB 2; Length 53;

Best Local Similarity 95.8%; Pred. No. 1.5e-28;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRRSVQWCAVSOPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 48
Db 1 GRRSVQWCAVSNPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 48

RESULT 14

US-08-406-271-5
Sequence 5, Application US/08406271
Patent No. 5919913
GENERAL INFORMATION:
APPLICANT: Nuyens, Jan H.
APPLICANT: Van Veen, Harry H.
TITLE OF INVENTION: Isolation of Lactoferrin from Milk
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: One Market Plaza, Steuart Street Tower, 20th
FLOOR
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,271
FILING DATE: 09-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,321
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-004910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..53
OTHER INFORMATION: /note= "HLF CDNA Rado"
US-08-406-271-5

Query Match 97.4%; Score 260; DB 2; Length 53;
Best Local Similarity 95.8%; Pred. No. 1.5e-28;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRRSVQWCAVSOPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 48
Db 1 GRRSVQWCAVSNPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 48

RESULT 15
US-09-017-043A-3
Sequence 3, Application US/09017043A
Patent No. 6333311
GENERAL INFORMATION:
APPLICANT: Nuijens, Jan
APPLICANT: van Berkel, Patrick

TITLE OF INVENTION: Useful Properties of Human Lactoferrin
and Variants Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,043A
FILING DATE: 02-FEB-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,859
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016994-011010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-017-043A-3

Query Match 95.1%; Score 254; DB 4; Length 52;
Best Local Similarity 95.7%; Pred. No. 9.5e-28;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSOPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 48
Db 3 RRRSVQWCAVSNPEATKCFQWQNNRKVRGPPVSCIKRDSPIQIOA 49

Search completed: September 1, 2004, 00:18:40
Job time : 31.04 secs

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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:15:50 ; Search time 109.44 Seconds
(without alignments)
137,988 Million cell updates/sec

Title: US-09-508-095-19

Perfect score: 267

Sequence: 1 GRRSVQWCAVSGPEATKCF.....VRGPPVSCIKRDSPIQICQA 48

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	97.8	690	14	US-10-076-816-4 Sequence 4, Appli
2	261	97.8	690	14	US-10-077-381-4 Sequence 4, Appli
3	261	97.8	690	16	US-10-639-835-4 Sequence 4, Appli
4	261	97.8	694	13	US-10-023-096-2 Sequence 2, Appli
5	261	97.8	711	14	US-10-169-297-9 Sequence 9, Appli
6	261	97.8	711	14	US-10-170-221-4 Sequence 4, Appli
7	261	97.8	711	15	US-10-341-434-202 Sequence 202, App
8	261	97.8	711	15	US-10-341-434-218 Sequence 69, Appli
9	261	97.8	711	15	US-10-440-464-63 Sequence 241, App
10	258	96.6	333	16	US-10-408-765A-441 Sequence 2, Appli
11	254	95.1	709	14	US-10-170-221-2 Sequence 2000, Ap
12	254	95.1	711	16	US-10-408-765A-2000 Sequence 20, Appli
13	142	53.2	25	10	US-09-798-869-28 Sequence 24, Appli
14	142	53.2	25	10	US-09-798-869-28 Sequence 8, Appli
15	129	48.3	708	14	US-10-169-297-8

16	118.5	44.4	164	9	US-09-738-973-203	Sequence 203, App
17	118.5	44.4	164	9	US-09-854-133-203	Sequence 203, App
18	118.5	44.4	164	14	US-10-144-649A-203	Sequence 203, App
19	118.5	44.4	679	12	US-10-384-060-3	Sequence 3, Appli
20	118.5	44.4	679	15	US-10-378-094-3	Sequence 3, Appli
21	118.5	44.4	679	16	US-10-211-494-3	Sequence 6, Appli
22	118.5	44.4	698	10	US-09-935-642-6	Sequence 10, Appli
23	118.5	44.4	698	12	US-10-383-201-10	Sequence 14, Appli
24	118.5	44.4	698	12	US-10-384-201-14	Sequence 2, Appli
25	118.5	44.4	698	15	US-10-378-094-2	Sequence 2, Appli
26	118.5	44.4	698	16	US-10-211-494-2	Sequence 2, Appli
27	118.5	44.4	1074	12	US-09-753-385-2	Sequence 4, Appli
28	118.5	44.4	1410	12	US-09-753-385-4	Sequence 693, App
29	118.5	39.9	255	10	US-09-866-050A-693	Sequence 55, Appli
30	106.5	39.9	698	12	US-10-205-311-55	Sequence 275, App
31	106.5	39.9	698	14	US-10-316-253-275	Sequence 273, App
32	106.5	39.9	698	14	US-10-316-253-273	Sequence 273, App
33	104.5	39.1	695	14	US-09-798-869-22	Sequence 26, Appli
34	96	36.0	25	10	US-09-798-869-23	Sequence 23, Appli
35	96	36.0	25	10	US-09-798-869-26	Sequence 27, Appli
36	90	33.7	25	10	US-09-798-869-27	Sequence 2, Appli
37	90	33.7	25	10	US-09-798-869-2	Sequence 2, Appli
38	87	32.6	15	10	US-09-798-869-1	Sequence 6, Appli
39	87	32.6	15	10	US-10-145-651-1	Sequence 6, Appli
40	86	32.2	17	14	US-09-798-869-6	Sequence 3, Appli
41	79	29.6	15	10	US-09-798-869-6	Sequence 6, Appli
42	79	29.6	15	10	US-10-133-642-3	Sequence 3, Appli
43	76.5	28.7	719	14	US-10-181-937-3	Sequence 102, App
44	76.5	28.7	738	12	US-09-847-208-102	
45	76	28.5	705	10		

ALIGNMENTS

RESULT 1
US-10-076-816-4
; Sequence 4, Application US/10076816
; Publication No. US2003005624A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodriguez, Raymond
; APPLICANT: Hagler, Frank B.
; TITLE OF INVENTION: Feed Additive Compositions and Methods
; FILE REFERENCE: 50665-8021.US00
; CURRENT APPLICATION NUMBER: US/10/076,816
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,188
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-816-4
Query Match 97.8%; Score 261; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 47; Conservative 0; Mismatches 0; Gaps 0;
OY 2 RRRSVQWCAVSGPEATKCFQWRMRKVRGPPVSCIKRDSPIQICQA 48
DB 3 RRRSVQWCAVSGPEATKCFQWRMRKVRGPPVSCIKRDSPIQICQA 49

US-10-077-381-4
; Sequence 4, Application US/10077381
; Publication No. US20030074700A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodriguez, Raymond
; APPLICANT: Hagie, Frank E.
; TITLE OF INVENTION: Expression of Human Milk Proteins in
; FILE REFERENCE: 50665-8022.US00
; CURRENT APPLICATION NUMBER: US/10/077,381
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,199
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-381-4

Query Match 97.8%; Score 261; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 1e-25; 0; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0;

QY 2 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 48
Db 3 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 49

RESULT 3
US-10-639-835-4
; Sequence 4, Application US/10639835
; Publication No. US2004011766A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodriguez, Raymond
; APPLICANT: Hagie, Frank E.
; TITLE OF INVENTION: Expression of Human Milk Proteins in
; FILE REFERENCE: 50665-8022.US01
; CURRENT APPLICATION NUMBER: US/10/639,835
; CURRENT FILING DATE: 2003-08-12
; PRIOR APPLICATION NUMBER: US 10/077,381
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,199
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-639-835-4

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Best Local Similarity 100.0%; Pred. No. 1e-25; 0; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 48

Db 3 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 49

RESULT 4
US-10-023-096-2
; Sequence 2, Application US/10023096
; Publication No. US20020160941A1
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Golinick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St., N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,586
; FILING DATE: 30-SEPT-1996
; APPLICATION NUMBER: US 08/238,445
; FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10505/P58185C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 694 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-023-096-2

Query Match 97.8%; Score 261; DB 13; Length 694;
Best Local Similarity 100.0%; Pred. No. 1e-25; 0; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0;

QY 2 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 48
Db 5 RRSVQWCAVSQPEATKCFQWQRMKRVGPPVSCIKRDSPIQICIA 51

RESULT 5
US-10-169-297-9
; Sequence 9, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
; APPLICANT: Tohach, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; TITLE OF INVENTION: Hepatitis
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: PCT/JP00/09393
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 11/374087
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-169-297-9

Query Match
Best Local Similarity 100.0%; Pred. No. 1,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 6
US-10-170-221-4
Sequence 4, Application US/10170221
Publication No. US20030192068A1
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/170,221
FILING DATE: 11-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-170-221-4

Query Match
Best Local Similarity 100.0%; Pred. No. 1,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 7
US-10-341-434-202
Sequence 202, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 202
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-202

Query Match
Best Local Similarity 100.0%; Pred. No. 1,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 8
US-10-341-434-218
Sequence 218, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 218
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-218

Query Match
Best Local Similarity 100.0%; Pred. No. 1,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSOPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 48

Db 22 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 9

US-10-440-464-69
; Sequence 69, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-69

Query Match 97.8%; Score 261; DB 15; Length 711;
Best Local Similarity 100.0%; Pred. No. 1.1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 2 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 48
Db 22 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 10
US-10-408-765A-241
; Sequence 241, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-241

Query Match 96.6%; Score 258; DB 16; Length 333;
Best Local Similarity 97.9%; Pred. No. 1.2e-25;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 2 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 48
Db 2 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 48

RESULT 11

US-10-170-221-2
; Sequence 2, Application US/10170221
; Publication No. US20030192068A1
; GENERAL INFORMATION:
; APPLICANT: DeBoer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,221
; FILING DATE: 11-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,798
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-170-221-2

Query Match 95.1%; Score 254; DB 14; Length 709;
Best Local Similarity 97.9%; Pred. No. 8.8e-25;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 48
Db 21 RRSVQWCAVSQPEATKCFQWQNMNRKVRGPPVSCIKRDSPIQIOA 67

RESULT 12
US-10-408-765A-2000
; Sequence 2000, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2000
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2000

Query Match 95.1%; Score 254; DB 16; Length 711;
Best Local Similarity 95.7%; Pred. No. 8.8e-25;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRRSVQWCAVSGPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 48
DB 22 RRRSVQWCTVSGPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 68

RESULT 13
US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
; APPLICANT: JOHN SIGURD SVENDSEN
; APPLICANT: VISTEIN REKDAL
; APPLICANT: BALDUR SVEINBJARNSSON
; APPLICANT: IARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; FILE REFERENCE: A34049-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/GB99/02851
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-869-20

Query Match 53.2%; Score 142; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TKCFQWQRMNRKVRGPPVSCIKRDS 41
DB 1 TKCFQWQRMNRKVRGPPVSCIKRDS 25

RESULT 14
US-09-798-026B-24
; Sequence 24, Application US/09798026B
; Publication No. US20030148936A1
; GENERAL INFORMATION:

; APPLICANT: ALPHARMA AS
; TITLE OF INVENTION: Cytotoxic Peptides Modified by Bulky or Lipophilic Moieties
; FILE REFERENCE: 40745.2
; CURRENT APPLICATION NUMBER: US/09/798,026B
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-026B-24

Query Match 53.2%; Score 142; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TKCFQWQRMNRKVRGPPVSCIKRDS 41
DB 1 TKCFQWQRMNRKVRGPPVSCIKRDS 25

RESULT 15
US-10-169-297-8
; Sequence 8, Application US/10169297
; Publication No. US20030171276A1
; GENERAL INFORMATION:
; APPLICANT: Tohdoh, Naoki
; APPLICANT: Murata, Masashi
; APPLICANT: Enjoji, Takashi
; TITLE OF INVENTION: Preventives and Remedies for Chronic
; FILE REFERENCE: 3435.1000-000
; CURRENT APPLICATION NUMBER: US/10/169,297
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/JP00/09393
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 11/374087
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-169-297-8

Query Match 48.3%; Score 129; DB 14; Length 708;
Best Local Similarity 43.2%; Pred. No. 2.7e-08;
Matches 19; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 3 RRSVQWCAVSGPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 46
DB 22 RRRSVQWCTVSGPEATKCFQWQRMNRKVRGPPVSCIKRDSPIQIOA 65

Search completed: September 1, 2004, 00:49:22
Job time: 110.44 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 00:03:45 ; Search time 27.84 Seconds
(without alignments)
165.847 Million cell updates/sec

Title: US-09-508-095-19

Perfect score: 267

Sequence: 1 GRRRSYQWCAVSGQPEATKCF.....VRGPVSCIKRDSPIQCIQA 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_78:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	97.8	711	1	TFHUL
2	162	60.7	708	1	lactotransferrin p
3	159	59.6	707	1	lactoferrin - goat
4	134	50.2	708	1	lactoferrin precu
5	132.5	49.6	704	2	lactotransferrin p
6	120	44.9	704	1	carbonic anhydrase
7	119.5	44.4	698	1	transferrin - pig
8	118	44.2	703	2	transferrin - pig
9	115	43.1	33	2	lactoferrin precu
10	110.5	41.4	694	1	lactoferrin - shue
11	104.5	39.1	695	2	transferrin precu
12	103	38.6	706	2	transferrin precu
13	76.5	28.7	64	2	transferrin - Acta
14	76.5	28.7	690	2	transferrin - Acta
15	76.5	28.7	738	1	transferrin - Acta
16	76	28.5	705	1	transferrin - Acta
17	72	27.0	717	2	transferrin - Acta
18	68	25.5	311	2	transferrin - Acta
19	62.5	22.5	551	2	transferrin - Acta
20	57	21.3	373	1	transferrin - Acta
21	57	21.3	373	2	transferrin - Acta
22	57	21.3	373	3	transferrin - Acta
23	56	21.0	262	2	transferrin - Acta
24	55	20.6	2505	1	transferrin - Acta
25	54	20.2	417	2	transferrin - Acta
26	54	20.2	419	2	transferrin - Acta
27	54	20.2	422	2	transferrin - Acta
28	53.5	20.0	1371	1	transferrin - Acta
29	53.5	20.0	1371	2	transferrin - Acta

30	53.5	20.0	3871	2	transferrin - Acta
31	53	19.9	170	2	transferrin - Acta
32	53	19.9	189	2	transferrin - Acta
33	53	19.9	370	1	transferrin - Acta
34	53	19.9	373	1	transferrin - Acta
35	53	19.9	373	2	transferrin - Acta
36	53	19.9	373	3	transferrin - Acta
37	52.5	19.7	388	2	transferrin - Acta
38	52.5	19.7	738	2	transferrin - Acta
39	52.5	19.7	820	2	transferrin - Acta
40	51.5	19.3	681	1	transferrin - Acta
41	51.5	19.3	811	2	transferrin - Acta
42	51.5	19.3	815	2	transferrin - Acta
43	51.5	19.3	1265	2	transferrin - Acta
44	51	19.1	274	2	transferrin - Acta
45	51	19.1	274	2	transferrin - Acta

ALIGNMENTS

RESULT 1
TFHUL
lactotransferrin precursor [validated] - human
N/Alternate names: lactoferrin
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C/Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
R/Chn: Y
submitted to the EMBL Data Library, March 1994
A/Reference number: G06820
A/Accession: G01394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-711 <CHO>
A/Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237
R/Ref: M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A/Reference number: S11228; MUID:90384839; PMID:2402455
A/Accession: S11228
A/Molecule type: mRNA
A/Residues: 1-148; T', 150-422; C', 424-711 <REV>
A/Cross-references: EMBL:X51961; NID:G34415; PIDN:CAA37914.1; PID:G34416
R/Ref: T'eng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A/Title: Differential molecular mechanism of the estrogen action that regulates lactofer
A/Reference number: A45401; MUID:93125571; PMID:1480183
A/Accession: A45401
A/Molecule type: DNA
A/Residues: 1-15 <TEN>
A/Cross-references: GB:52659; NID:G263311; PIDN:AAB24877.1; PID:G263312
A/Experimental source: Placenta
A/Note: sequence extracted from NCBI backbone (NCBI:122202)
R/Powell, M.J.; Ogden, J.E
Nucleic Acids Res. 18, 4013, 1990
A/Title: Nucleotide sequence of human lactoferrin cDNA.
A/Reference number: S10324; MUID:90326549; PMID:2374794
A/Accession: S10324
A/Molecule type: mRNA
A/Residues: 3-711 <POW>
A/Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412
R/Ref: Stowell, K.W.; Rado, T.A.; Funk, W.D.; Tweede, J.W.
Biochem. J. 276, 349-355, 1991
A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A/Reference number: S15853; MUID:91264786; PMID:2049066
A/Accession: S15853
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 20-31 <ST1>
A/Accession: S20841
A/Molecule type: protein
A/Residues: 20-28; X', 30-31 <ST2>

R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A:Reference number: S07160; MUID:88001031; PMID:3477300
 A:Accession: S07160
 A:Molecule type: mRNA
 A:Residues: 436-487, 'A', 489-711 <RAD>
 A:Cross-References: EMBL:M18642; NID:g186815; PIDN:AAA6665.1; PID:g386855
 R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; MUID:91235214; PMID:1674448
 A:Accession: A61169
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 3-701, 'SMKPVN' <PAN>
 A:Experimental source: normal breast tissue
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
 Eur. J. Biochem. 145, 659-666, 1984
 A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A:Reference number: A31000; MUID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A>Note: this is the final paper in a series
 R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity
 A:Reference number: S74119; MUID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:LTf
 A:Cross-References: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-711/Product: lactotransferrin #status experimental <MAT>
 F:21-366/Domain: transferrin repeat homology <TRH1>
 F:361-699/Domain: transferrin repeat homology <TRH2>
 F:729-65, 35-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
 F:157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat
 Query Match 97.8%; Score 261; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 3, 7e-25;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRSVOMCAVSOEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48
 Db 22 RRSVOMCAVSOEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 68

RESULT 2
 JCO2323
 lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JCO2323
 R:Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A:Reference number: JCO2323; MUID:94380047; PMID:8093048
 A:Accession: JCO2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 60.7%; Score 162; DB 2; Length 708;
 Best Local Similarity 52.2%; Pred. No. 1, 2e-12;
 Matches 24; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 3 RRSVOMCAVSOEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48
 Db 22 RRSVOMCAVSOEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 67

RESULT 3
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-References: EMBL:J03298
 R:Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LU>
 A:Cross-References: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-685/Domain: transferrin repeat homology <TRH2>
 F:499/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.6%; Score 159; DB 1; Length 707;
 Best Local Similarity 61.4%; Pred. No. 2, 9e-12;
 Matches 27; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 5 SVOMCAVSOEATKCFQWQNMKRVGPPVSCIKRDSPIQIOA 48
 Db 23 TWRMCAVSNSEERKCFQWQNMKRVGPPVSCIKRDSPIQIOA 66

RESULT 4
 TFBOL
 lactotransferrin precursor - bovine
 N:Alternate names: lactoferrin
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 11-May-2000
 C:Accession: I45919; S14674; S14110; S18517; J05955; S13097; S18518; S13881; P10148; S21
 R:Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A:Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein fr
 A:Reference number: I45919
 A:Accession: I45919
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-708 <TSA>
 A:Cross-References: GB:I08604; NID:g163269; PIDN:AAA30609.1; PID:g163270
 R:Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S14674
 A:Accession: S14674
 A:Molecule type: mRNA
 A:Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI>
 A:Cross-References: EMBL:X57084; NID:G505; PIDN:CAA40366.1; PID:G505
 R:Pierce, A.; Colavizza, D.; Benalissa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G

Eur. J. Biochem. 196, 177-184, 1991
 A>Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A/Reference number: S14110; MUID:91165550; PMID:2001696
 A/Accession: S14110
 A/Molecule type: mRNA
 A/Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A/Cross-references: EMBL:X57084
 A/Accession: S18517
 A/Molecule type: protein
 A/Residues: 20-35/82-114/148-163, 'P', 166-178, 'V', 'P', 183-190/205-212/230-239/304-339/59
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A>Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
 A/Reference number: J0595; MUID:92028986; PMID:1718281
 A/Accession: J0595
 A/Molecule type: mRNA
 A/Residues: 1-65, 'P', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A/Cross-references: GB:M63502
 A/Note: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 R/Mead, P.E.; Tweedie, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A>Title: cDNA and protein sequence of bovine lactoferrin.
 A/Reference number: S13097; MUID:91088328; PMID:2263492
 A/Accession: S13097
 A/Molecule type: mRNA
 A/Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A/Cross-references: EMBL:X54801
 A/Accession: S18518
 A/Molecule type: protein
 A/Residues: 20-47/59-66/132-139/256-277/278, 305-332/343-351/361-363/586, 587-589/598-619
 R/Mead, P.E.
 Submitted to the EMBL Data Library, October 1990
 A/Reference number: S13881
 A/Accession: S13881
 A/Molecule type: mRNA
 A/Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
 A/Cross-references: EMBL:X54801
 R/Reifman, J.J.; Hegarty, H.M.; Hurley, M.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A>Title: Purification and characterization of bovine lactoferrin from secretions of the
 A/Reference number: P10148; MUID:90031466; PMID:2805645
 A/Accession: P10148
 A/Molecule type: protein
 A/Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R/Bellamy, W.; Takase, M.; Yamauchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A>Title: Identification of the bactericidal domain of lactoferrin.
 A/Reference number: S21756; MUID:92287941; PMID:1599334
 A/Accession: S21756
 A/Molecule type: protein
 A/Residues: 36-60 <BEL>
 R/Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A>Title: Separation and characterization of the C-terminal half molecule of bovine lacto
 A/Reference number: A56659; MUID:93253156; PMID:8488845
 A/Accession: A56659
 A/Molecule type: protein
 A/Residues: 20-25/302-308/359-366, 'X', 368-376, 'X', 378 <SHI>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F1-19/Domains: signal sequence #status predicted <SIG>
 F1-20-708/Product: lactotransferrin #status predicted <MAT>
 F1-20-355/Domains: transferrin repeat homology <TRH1>
 F1-36-60/Region: antimicrobial
 F1-359-696/Domains: transferrin repeat homology <TRH2>
 F1-38-64/134-217/176-192/179-200/189-202/250-264/367-399/377-390/424-703/444-666/476-551,
 F1-38-55/Disulfide bonds: #status predicted
 F1-79, 111, 211, 272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F1-140/Binding site: carbonate (Arg) #status experimental
 F1-252, 300, 387, 495, 564/Binding site: carboxylate (Asn) (covalent) #status predicted
 F1-414, 452, 545, 614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F1-482/Binding site: carbonate (Arg) #status experimental

Query Match 50.2%; Score 134; DB 1; Length 708;
 Best Local Similarity 43.5%; Pred. No. 4, 2e-09;
 Matches 20; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 Db 22 RRVNMCITISQPEWFKCRNQMFKKGCAPBITCVRAFALECIIRA 67
 3 RRSVQMCASQPEATKCFQWQNRNKGPPVSCIKRDSPIQICQA 48
 147228
 caobonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
 C/Accession: I47228
 R/Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from por
 A/Reference number: I47228; MUID:93099129; PMID:11463741
 A/Accession: I47228
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-704 <ROU>
 A/Cross-references: EMBL:U36916; MUID:91016329; PIDN:AMB58956.1; PID:G1016330
 C/Genetics: A/Gene: PICA
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication
 F1-20-350/Domains: transferrin repeat homology <TRH1>
 Query Match 49.6%; Score 132.5; DB 2; Length 704;
 Best Local Similarity 49.0%; Pred. No. 6, 5e-09;
 Matches 24; Conservative 11; Mismatches 11; Indels 3; Gaps 1;
 Db 22 KETVRCWCTVSSQSEASKCSFRHNMKILPVEGPHVSQVKATSYLECIIRA 70
 3 RRSVQMCASQPEATKCFQWQNRNKGPPVSCIKRDSPIQICQA 48
 S01384
 transferrin - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 11-May-2000
 C/Accession: S01384; A60520; A61573
 R/Baldwin, G.S.; Weinstein, J.
 Nucleic Acids Res. 16, 8720, 1988
 A>Title: Nucleotide sequence of porcine liver transferrin.
 A/Reference number: S01384; MUID:88355629; PMID:3419934
 A/Accession: S01384
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-696 <BAL>
 A/Cross-references: EMBL:X12366; MUID:92126; PIDN:CAA30943.1; PID:9833800
 A/Note: 308-Arg was also found
 R/Baldwin, G.S.; Bacic, T.; Chandler, R.; Gregg, B.; Pedersen, J.; Simpson, R.J.; Toh, B
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A>Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine s
 A/Reference number: A60520; MUID:90227903; PMID:2328566
 A/Accession: A60520
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-11, 'X', 13-15 <BA2>
 A/Experimental source: gastric mucosa
 A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta
 R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A/Reference number: A61573; MUID:91293379; PMID:2065820
 A/Accession: A61573
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-18, 'XE' <CHU>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; plasma

A: Molecule type: protein

A;Residues: 1-695 <ES2>
A;Cross-references: EMBL:X77158; NID:G510195; PIDN:CAAS4403.1; PID:G510196

Best Local Similarity 32.6%; Pred. No. 0.078;
Matches 14; Conservative 8; Mismatches 16; Indels 5; Gaps 1;

OY 6 VQMCVSPQEPATKCFQWQNNRKYRGPPVSCIKRDSPIQCIQ 48
DB 25 VKMCVKSEQLRKCHDLAAKVAE----FSCVRKDGSEFCIQ 62

RESULT 15

TFHUM

melanotransferrin precursor - human

N:Alternate names: melanoma-associated antigen gp95/p97

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-Jan-2000

C:Accession: A23814; A60925

R:Rose, T.M.; Picman, G.D.; Teplow, D.B.; Dreyer, W.J.; Hellstrom, K.E.; Brown, J.P.

Proc. Natl. Acad. Sci. U.S.A. 83, 1261-1265, 1986

A:Title: Primary structure of the human melanoma-associated antigen p97 (melanotransferrin)

A:Reference number: A23814; MUID:86149285; PMID:2419904

A:Accession: A23814

A:Molecule type: mRNA

A:Residues: 1-738 <ROS>

A:Cross-references: EMBL:M2154; NID:G189515; PID:AAA5992.1; PID:G189518

A:Experimental source: melanoma

R:Funakawa, K.S.; Funakawa, K.; Real, F.X.; Old, L.J.; Lloyd, K.O.

J. Exp. Med. 169, 585-590, 1989

A:Title: A unique antigenic epitope of human melanoma is carried on the common melanoma

A:Reference number: A60925; MUID:8904252; PMID:2463331

A:Accession: A60925

A:Molecule type: protein

A:Residues: 20-25, 'X', 27-28, 'X', 30 <FUR>

C:Comment: This protein is found predominantly in human melanomas and in certain fetal

C:Comment: Seven disulfide bonds are predicted in each domain.

C:Genetics:

A:Gene: GDB:MF12

A:Cross-references: GDB:119387; OMIM:155750

A:Map position: 3q28-3q29

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: blocked carboxyl end; duplication; glycoprotein; lipoprotein; membrane prote

F:1-19/Domain: signal sequence #status predicted <SIG>

F:18-360/Domain: transferrin repeat homology <TRH>

F:20-710/Product: melanotransferrin #status predicted <MTP>

F:361-709/Domain: transferrin repeat homology <TRH2>

F:711-738/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:28,135,515/Binding site: carboxylate (Asn) (covalent) #status predicted

F:710/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 28.7%; Score 76.5; DB 1; Length 738;

Best Local Similarity 32.6%; Pred. No. 0.082; Mismatches 20; Indels 1; Gaps 1;

Matches 14; Conservative 8; Mismatches 20; Indels 1; Gaps 1;

OY 6 VQMCVSPQEPATKCFQWQNNRKYRGPPVSCIKRDSPIQCIQ 47
DB 366 LKMCVSLSTPEIQKCGDMVAVFRQRRLKPEIQCVSAKSPQHME 408

Search completed: September 1, 2004, 00:17:06
Job time : 29.84 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:44 / Search time 16.32 Seconds

(without alignments)
153.148 Million cell updates/sec

Title: US-09-508-095-19

Perfect score: 267
Sequence: 1 GRRRSYQWCAVSGPEATKCF.....VRGPVSCIKRDSPIQICQA 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261	97.8	711	1 TRFL_HUMAN	P02788 homo sapien
2	164	61.4	695	1 TRFL_HORSE	O77811 equus caball
3	163	61.0	708	1 TRFL_CAPRI	Q29477 capra hircu
4	162	60.7	708	1 TRFL_CAMDR	Q9tumo camelus dro
5	159	59.6	707	1 TRFL_MOUSE	P08571 mus musculu
6	136	50.9	708	1 TRFL_BUBBU	O77698 bubalus bub
7	134	50.2	708	1 TRFL_BOVIN	F24627 bos taurus
8	132.5	49.6	704	1 ICA_PIG	Q29545 sus scrofa
9	120	44.9	696	1 TRFE_PIG	P09571 sus scrofa
10	118.5	44.4	698	1 TRFE_HUMAN	P02787 homo sapien
11	118	44.2	704	1 TRFL_PIG	P14632 sus scrofa
12	112	41.9	704	1 TRFE_RABIT	Q29443 bos taurus
13	110.5	41.4	685	1 TRFE_RABIT	P19134 oryctolagus
14	106.5	39.9	687	1 TRFE_MOUSE	Q92111 mus musculu
15	106.5	39.9	698	1 TRFE_RAT	P12346 rattus norv
16	103	38.6	706	1 TRFE_HORSE	P27425 equus caball
17	85.5	32.0	687	1 TRFE_ONCHI	P79815 onchornychu
18	77.5	29.0	686	1 TRFE_ANAPL	P56410 anas platyr
19	76.5	28.7	690	1 TRFE_SALSA	P80426 salmo salar
20	76.5	28.7	691	1 TRFE_SALSA	P80429 salmo salar
21	76.5	28.7	738	1 TRFE_HUMAN	P08582 homo sapien
22	76	28.5	705	1 TRFE_PAROL	O93429 parallachth
23	75.5	28.3	738	1 TRFE_CHICK	P02789 gallus galli
24	73.5	27.5	690	1 TRFE_MOUSE	O92079 gadus moru
25	73.5	27.5	690	1 TRFE_MOUSE	P12785 rattus norv
26	72	27.3	844	1 SAY_RANCA	P34692 caenorhabdi
27	72	27.0	701	1 TRFE_ORYLA	P79919 cryzias lat
28	57	21.3	373	1 TRFE_XENLA	P31426 rana catesb
29	57	21.3	546	1 TRFE_XENLA	P20233 xenopus lae
30	57	21.3	546	1 TRFE_XENLA	P20233 xenopus lae
31	55	20.6	2505	1 TRFE_GADMO	Q17865 caenorhabdi
32	54	20.2	422	1 U163_CAEEL	P34692 caenorhabdi
33	53.5	20.0	1371	1 VCAP_HSVSA	Q00399 herpesvirus

ALIGNMENTS

34	53	19.9	137	1 CS11_HUMAN	Q9h112 homo sapien
35	53	19.9	373	1 TYRA_ECOLI	P07023 escherichia
36	52.5	19.7	64	1 BD01_CAPRI	O97946 capra hircu
37	52.5	19.7	738	1 I12R_MOUSE	Q60837 mus musculu
38	52.5	19.7	2130	1 BAZB_CHICK	Q9d413 gallus galli
39	52	19.5	333	1 AMP_IMPBA	O24006 i antimicro
40	51.5	19.3	681	1 TRF_MANSE	P22297 manduca sex
41	51.5	19.3	811	1 SYO_SCHPO	O9y7y8 schizosacch
42	51.5	19.3	1265	1 MVOF_MOUSE	Q64331 mus musculu
43	51	19.1	274	1 MOVF_TMOB	Q83485 todonovirus
44	51	19.1	522	1 POLS_RUBV	P08564 rubella vir
45	50.5	18.9	525	1 LAG3_HUMAN	P18627 homo sapien

RESULT 1

ID	TRFL_HUMAN	STANDARD;	PRT;	711 AA.
AC	P02788; O00756; Q16780; Q16785; Q16789; Q26KZ4; Q26KZ5;			
AC	Q9H123;			
DT	21-JUL-1996 (Rel. 01, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Lactoferrin precursor (Lactoferrin) [Contains: Lactoferrin A; Lactoferrin B; Lactoferrin C].			
GN	LTF OR LF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RX	MEDLINE=90384839; PubMed=2402455;			
RA	Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.,			
RT	"Complete nucleotide sequence of human mammary gland lactoferrin";			
RL	Nucleic Acids Res. 18:5288-5288 (1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Choi Y.Y.;			
RT	Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	Connely O.M.;			
RA	Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Liang Q., Jimenez-Flores R., Richardson T.;			
RT	"Molecular cloning and sequence analysis of human lactoferrin";			
RL	Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RA	Wei X., Han J., Rado T.A.;			
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA sequences";			
RL	Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Mammary gland;			
RA	Cheng H., Chen X., Huan L.;			
RT	"cDNA Cloning and sequence analysis of human lactoferrin";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.L., Reingold B.A., Grouse L.H., Derge J.G.,			
RT	MEHLIN=22388257; PubMed=12477932;			
RL	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasel F.,
 RA Stachewicz L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachewicz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carrino R.D., Mullany S.J.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abrahamson R.D., Guntaratne P.H.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gay L.J., Hultx S.W.,
 RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodighiero S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Alakselä R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [8]
 RP SEQUENCE OF 3-711 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=90326549; PubMed=2374734;
 RA Powell M.J., Oden J.E.;
 RL "Nucleotide sequence of human lactoferrin cDNA.";
 RL Nucleic Acids Res. 18:4013-4013(1990).
 RL [9]
 RP SEQUENCE OF 20-711.
 RX MEDLINE=9076667; PubMed=6510420;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
 RA Legend D., Spik G., Montreuil J., Jolles P.;
 RL "Human lactoferrin: amino acid sequence and structural
 RT comparisons with other transferrins.";
 RL Eur. J. Biochem. 145:659-666(1984).
 RL [10]
 RP PEBLIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
 RX MEDLINE=82046817; PubMed=6794640;
 RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
 RA Jolles P.;
 RL "The present state of the human lactoferrin sequence. Study and
 RT alignment of the cyanogen bromide fragments and characterization of
 RL N- and C-terminal domains.";
 RL Biochim. Biophys. Acta 670:243-254(1981).
 RL [11]
 RP SEQUENCE OF 609-711.
 RX MEDLINE=82262043; PubMed=7049727;
 RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
 RA Jolles P.;
 RL "An 88 amino acid long C-terminal sequence of human
 RT lactoferrin.";
 RL FEBS Lett. 142:107-110(1982).
 RL [12]
 RP SEQUENCE OF 436-711 FROM N.A.
 RX MEDLINE=88001031; PubMed=3477300;
 RA Rado T.A., Wei X., Benz E.J., Jr.;
 RL "Isolation of lactoferrin cDNA from a human myeloid library and
 RT expression of mRNA during normal and leukemic myelopoiesis.";
 RL Blood 70:989-993(1987).
 RL [13]
 RP SEQUENCE OF 237-711 FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nman M., Pannell L., Dedhia N., Ansari A., Mardis E., Schultz K.,
 RA Guo J., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
 RA Sargent J.L.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RL [14]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
 RX MEDLINE=90064528; PubMed=2585506;
 RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
 RL "Structure of human lactoferrin: crystallographic structure analysis
 RT and refinement at 2.8-A resolution.";

RL J. Mol. Biol. 209:711-734(1989).
 RL [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RA Haidas M., Anderson B.F., Baker E.N.;
 RL "Structure of human dimeric lactoferrin refined at 2.2-A
 RT resolution.";
 RL Acta Crystallogr. D 51:629-646(1995).
 RL [16]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
 RX MEDLINE=97156796; PubMed=9003186;
 RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
 RA Baker E.N.;
 RL "Maturation of the histidine ligand in human lactoferrin: iron
 RT binding properties and crystal structure of the histidine-
 RL 253--methionine mutant.";
 RL Biochemistry 36:341-346(1997).
 RL [17]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=99190892; PubMed=10089347;
 RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
 RL "Structure of recombinant human lactoferrin expressed in Aspergillus
 RT awamori.";
 RL Acta Crystallogr. D 55:403-407(1999).
 RL [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99192677; PubMed=10089508;
 RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
 RL "Structure of human apolactoferrin at 2.0-A resolution. Refinement
 RT and analysis of ligand-induced conformational change.";
 RL Acta Crystallogr. D 54:1339-1335(1998).
 RL [19]
 RP CHARACTERIZATION OF LACTOFERROXINS.
 RX MEDLINE=91166929; PubMed=1365293;
 RA Tanl F., Ito K., Chiba H., Yoshikawa M.;
 RL "Isolation and characterization of oploid antagonist peptides derived
 RT from human lactoferrin.";
 RL Agric. Biol. Chem. 54:1803-1810(1990).
 RL [20]
 RP VARIANTS THR-30 AND ARG-48.
 RX MEDLINE=99091914; PubMed=9873069;
 RA Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
 RA Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotia Y.,
 RA Sugar J., Kumaraswamykavel G., Munier F., Schorderet D.F.,
 RA El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
 RA Hejtmancik J.F., Teng C.T.;
 RL "Familial subepithelial corneal amyloidosis (gelatinous drop-like
 RT corneal dystrophy): exclusion of linkage to lactoferrin gene.";
 RL Mol. Vision 4:31-32(1998).
 RL [21]
 RP FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION. USUALLY BICARBONATE.
 CC FUNCTION: LACTOFERROXINS A, B AND C HAVE OPTOID ANTAGONIST
 CC ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
 CC LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
 CC FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 CC -----
 CC EMBL, X53961; CAA37914.1; -;
 CC EMBL, U07643; AAB60324.1; -;
 CC EMBL, M93150; AAB36159.1; -;
 CC EMBL, M83202; AAB59511.1; -;
 CC EMBL, M83205; AAB58656.1; -;

Query Match 97.8%; Score 261; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 6,7e-26;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRSVOMCAVSQPEATKCFOWOMNRKRVGSPVSCIKRDSPIQICQA 48
 |||||
 DB 22 RRSVOMCAVSQPEATKCFOWOMNRKRVGSPVSCIKRDSPIQICQA 68

RESULT 2
 TRFL HORSE STANDARD; PRT; 695 AA.

AC 077811;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin) (Fragment).
 GN LTF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;

NP SEQUENCE FROM N.A.
 RA Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "cDNA sequence of mare lactoferrin."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC TISSUE=Milk;
 RX MEDLINE=99296631; PubMed=1036507;
 RA Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
 RT "Three-dimensional structure of mare ferric lactoferrin at 2.6-A
 resolution.";
 RL J. Mol. Biol. 289:303-317(1999).

CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 OF AN ANION, USUALLY BICARBONATE.

CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AJ010930; CAA09407.1; -

DR PDB; 1B1X; 02-DEC-98.
 DR PDB; 1B7U; 02-FEB-99.
 DR PDB; 1B7Z; 02-FEB-99.
 DR PDB; 1F9B; 10-FEB-01.
 DR PDB; 1F9B; 13-FEB-02.
 DR PDB; 1QJW; 14-JAN-00.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: PF00405; transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_PFR_2

DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 KM Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KW Signal; 3d-structure.

FT SIGNAL 1
 FT CHAIN <1 6
 FT CHAIN 7 695 LACTOTRANSFERRIN.
 FT REPEAT 7 350 1.
 FT REPEAT 351 695 2.

FT DISULFID 15
 FT DISULFID 25
 FT DISULFID 121
 FT DISULFID 163
 FT DISULFID 166
 FT DISULFID 176
 FT DISULFID 237
 FT DISULFID 251
 FT DISULFID 354
 FT DISULFID 377
 FT DISULFID 411
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 FT DISULFID 463
 FT DISULFID 487
 FT DISULFID 497
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 FT DISULFID 631
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 FT METAL 259
 FT METAL 401
 FT METAL 439
 FT METAL 439
 FT METAL 532
 FT METAL 601
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 FT BINDING 129
 FT BINDING 130
 FT BINDING 130
 FT BINDING 465
 FT BINDING 469
 FT BINDING 471
 FT BINDING 471
 FT CARBOHYD 472
 FT CARBOHYD 143
 FT CARBOHYD 287
 FT CARBOHYD 482
 FT STRAND 12
 FT HELIX 19
 FT TURN 34
 FT STRAND 35
 FT STRAND 40
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 FT TURN 48
 FT TURN 57
 FT STRAND 62
 FT STRAND 65
 FT HELIX 74
 FT TURN 76
 FT STRAND 80
 FT STRAND 88
 FT STRAND 95
 FT STRAND 95
 FT STRAND 105
 FT TURN 106
 FT HELIX 107
 FT HELIX 112
 FT TURN 114
 FT STRAND 116
 FT TURN 117
 FT STRAND 122
 FT TURN 125
 FT TURN 126
 FT HELIX 128
 FT HELIX 131
 FT HELIX 137
 FT HELIX 139
 FT TURN 142
 FT HELIX 147
 FT STRAND 151
 FT TURN 158
 FT STRAND 161
 FT TURN 163
 FT TURN 166
 FT HELIX 169
 FT TURN 171
 FT HELIX 173
 FT TURN 175
 FT TURN 176
 FT TURN 178
 FT TURN 183
 FT TURN 187
 FT TURN 191
 FT TURN 192
 FT TURN 194
 FT HELIX 197
 FT HELIX 206
 FT TURN 207
 FT STRAND 212
 FT STRAND 216
 FT HELIX 219
 FT HELIX 223
 FT HELIX 227
 FT TURN 231
 FT STRAND 232
 FT STRAND 237

IRON 1.
 IRON 1.
 IRON 1.
 IRON 1.
 IRON 2.
 IRON 2.
 IRON 2.
 CARBONATE 1.
 CARBONATE 1.
 CARBONATE 1.
 CARBONATE 1 (VIA AMIDE NITROGEN).
 CARBONATE 1 (VIA AMIDE NITROGEN).
 CARBONATE 1 (VIA AMIDE NITROGEN).
 CARBONATE 2.
 CARBONATE 2 (VIA AMIDE NITROGEN).
 CARBONATE 2 (VIA AMIDE NITROGEN).
 CARBONATE 2 (VIA AMIDE NITROGEN).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).


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FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (BY SIMILARITY).
FT BINDING 484 484 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 485 485 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 56 56 I -> V (IN REF. 2).
FT CONFLICT 88 88 L -> R (IN REF. 2).
FT CONFLICT 124 124 Q -> K (IN REF. 2).
FT CONFLICT 154 154 F -> P (IN REF. 2).
FT CONFLICT 304 304 S -> R (IN REF. 2).
FT CONFLICT 414 414 D -> G (IN REF. 2).
SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C8353966D CRC64;

Query Match 61.0%; Score 163; DB 1; Length 708;
Best Local Similarity 54.3%; Pred. No. 2,5e-13;
Matches 25; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Cy 3 RRSVQWCAVSQPEATKCFQGNRMKRYGPPVCIKSDPSICIOA 48
Db 22 RKNVRWCATISLPWCKCYQWQRMKRLGAPSTICIRTSLEICIRA 67

RESULT 4
TRFL CAMDR STANDARD; PRT; 708 AA.
AC 09TUNG; O9MZSS;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Lactoferrin precursor (Lactoferrin).
GN Lf.
OS Camelus dromedarius (Dromedary) (Arabic camel).
OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9638;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Small; TISSUE=Lactating mammary gland;
RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
RL Int. Dairy J. 9:481-486 (1999).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Paramesivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).

```

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CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
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CC -----
CC EMBL; AJ131674; CAB53387.1; -.
CC EMBL; AF165879; AAF82241.1; -.
CC PDB; 1DTZ; 20-JUN-01.
CC InterPro; IPR001156; Transferrin.
CC Pfam; PF00405; transferrin.
CC PRINTS; PR00422; TRANSFERRIN.
CC SMART; SM00094; TR_FER; 2.
CC PROSITE; PS00205; TRANSFERRIN_1; 2.
CC PROSITE; PS00206; TRANSFERRIN_2; 2.
CC PROSITE; PS00207; TRANSFERRIN_3; 2.
CC Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
CC Signal; 3d-structure.
CC KW 1
CC FT 19 BY SIMILARITY.
FT CHAIN 20 708 LACTOTRANSFERRIN.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55 BY SIMILARITY.
FT DISULFID 124 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
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FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 694 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1 (BY SIMILARITY).
FT METAL 111 111 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 452 452 IRON 2 (BY SIMILARITY).
FT METAL 545 545 IRON 2 (BY SIMILARITY).
FT METAL 614 614 IRON 2 (BY SIMILARITY).
FT BINDING 140 140 CARBONATE 1 (BY SIMILARITY).
FT BINDING 142 142 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 143 143 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (BY SIMILARITY).
FT BINDING 484 484 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT BINDING 485 485 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 261 261 F -> S (IN REF. 2).
FT CONFLICT 304 304 G -> A (IN REF. 2).
FT CONFLICT 330 330 S -> P (IN REF. 2).
FT CONFLICT 492 494 LLS -> PLF (IN REF. 2).

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FT	TURN	251	252
FT	STRAND	255	257
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FT	STRAND	273	277
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FT	TURN	312	313
FT	TURN	321	322
FT	STRAND	325	328
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FT	HELIX	354	352
FT	STRAND	364	369
FT	HELIX	371	384
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FT	HELIX	415	422
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FT	TURN	438	441
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FT	TURN	603	605
FT	STRAND	609	611
FT	STRAND	615	619
FT	HELIX	620	637
FT	TURN	639	640
FT	TURN	642	647
FT	TURN	650	651
FT	TURN	654	655

Query Match 50.9%; Score 136; DB 1; Length 708;
 Best Local Similarity 43.5%; Pred. No. 7.2e-10;

Matches	20;	Conservative	14;	Mismatches	12;	Indels	0;	Gaps	0;
Cy	3	RRSVOMCAVSOPEATKCFQMRNMRKVRGPPVSCIKRDSPIOQA	48						
Db	22	RKNVWCTISQPEWLKCHRWQMKKLGAPSLTCVRAFLVCIRA	67						
RESULT 7									
TRFL_BOVIN		STANDARD;	PRT;	708 AA.					
ID	277	AC	P24627; Q29629; Q9WZV3;						
DT	01-MAR-1992	(Rel. 21, Created)							
DT	01-OCT-1993	(Rel. 27, Last sequence update)							
DT	10-OCT-2003	(Rel. 42, Last annotation update)							
DE	Lactoferrin precursor (lactoferrin) [Contains: Lactoferricin B (LFCIN B)].								
GN	LTP.								
OS	Bos taurus (Bovine).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;								
OC	Bovidae; Bovinae; Bos.								
OX	NCBI_TaxID=9913;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Submaxillary gland;								
RX	MEDLINE=91160550; PubMed=2001696;								
RA	Pierce A., Colavizza D., Benaissa M., Maes P., Tartar A.,								
RT	Montreuil J., Spik G.;								
RL	"Molecular cloning and sequence analysis of bovine lactotransferrin.";								
RL	Eur. J. Biochem. 196;177-184(1991).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=92028986; PubMed=718281;								
RA	Goodman R.B., Schanbacher F.L.;								
RT	"Bovine lactoferrin mRNA: sequence, analysis, and expression in the								
RL	mammary gland.";								
RL	Biochem. Biophys. Res. Commun. 180:75-84(1991).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Lung;								
RA	Tsang T.C., Burns D.K., Wang F., Pan Y.C.B., Schmidt A.M., Stern D.;								
RT	"Cloning of a 80-kD advanced glycosylation end product (AGE) binding								
RL	protein from bovine lung.";								
RL	FASEB J. 6:233-233(1991).								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Blood, and Mammary gland;								
RX	MEDLINE=94266164; PubMed=8206385;								
RA	Seyfert H.-W., Tuckoricz A., Interthal H., Koczan D., Hobom G.;								
RT	"Structure of the bovine lactoferrin-encoding gene and its promoter.";								
RL	Gene 143:265-269(1994).								
RN	[5]								
RP	SEQUENCE FROM N.A.								
RA	Nakamura I., Shimazaki K., Yagi Y., Watanabe A.;								
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.								
RN	[6]								
RP	SEQUENCE OF 20-59.								
RX	MEDLINE=90031466; PubMed=2805645;								
RA	Rejman J.J., Hegarty H.M., Hurley W.L.;								
RT	"Purification and characterization of bovine lactoferrin from								
RT	secretions of the involuting mammary gland: identification of								
RT	multiple molecular weight forms.";								
RL	Comp. Biochem. Physiol. 93B:929-934(1999).								
RN	[7]								
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).								
RX	MEDLINE=98062367; PubMed=9398529;								
RA	Moore S.A., Anderson B.F., Groom C.R., Haridas M., Baker E.N.;								
RT	"Three-dimensional structure of ferritin bovine lactoferrin at 2.8-A								
RL	resolution.";								
RL	J. Mol. Biol. 274:222-236(1997).								
RN	[8]								
RP	STRUCTURE BY NMR OF 36-60.								
RX	MEDLINE=98190007; PubMed=9521752;								

RA Hwang P.M., Zhou N., Arrowmitch C.H., Vogel H.J.;
RT "Three-dimensional solution structure of lactoferrin B, an
RT Antimicrobial peptide derived from bovine lactoferrin.",
RL Biochemistry 37:4288-4298(1998).
CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
CC -1- SUBUNIT: LACTOFERRICIN B IS AN ANTIMICROBIAL PEPTIDE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
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CC -----
DR EMBL; X57084; CAA40366.1; -;
DR EMBL; M63502; AAA30617.1; -;
DR EMBL; L08604; AAA30609.1; -;
DR EMBL; L19993; AAA21722.1; -;
DR EMBL; L19982; AAA21722.1; JOINED.
DR EMBL; L19983; AAA21722.1; JOINED.
DR EMBL; L19984; AAA21722.1; JOINED.
DR EMBL; L19985; AAA21722.1; JOINED.
DR EMBL; L19986; AAA21722.1; JOINED.
DR EMBL; L19988; AAA21722.1; JOINED.
DR EMBL; L19989; AAA21722.1; JOINED.
DR EMBL; L19990; AAA21722.1; JOINED.
DR EMBL; L19991; AAA21722.1; JOINED.
DR EMBL; L19992; AAA21722.1; JOINED.
DR EMBL; AB046664; BAB03470.1; -;
DR PIR; I45919; TFBOL.
DR PDB; 1BRF; 03-DEC-97.
DR PDB; 1LFC; 18-NOV-98.
DR GlycoSuiteDB; P24627; -;
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SMO0094; TR_PRR_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; Antibiocytic; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 1 708 LACTOTRANSFERRIN.
FT PEPTIDE 36 60 LACTOFERRICIN B.
FT REPEAT 20 363 1.
FT REPEAT 364 708 2.
FT DISULFID 28 64 BY SIMILARITY.
FT DISULFID 38 55
FT DISULFID 134 217 BY SIMILARITY.
FT DISULFID 176 192 BY SIMILARITY.
FT DISULFID 189 200 BY SIMILARITY.
FT DISULFID 250 264 BY SIMILARITY.
FT DISULFID 367 399 BY SIMILARITY.
FT DISULFID 377 390 BY SIMILARITY.
FT DISULFID 424 703 BY SIMILARITY.
FT DISULFID 444 666 BY SIMILARITY.
FT DISULFID 476 551 BY SIMILARITY.
FT DISULFID 500 624 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 521 534 BY SIMILARITY.
FT DISULFID 592 606 BY SIMILARITY.
FT DISULFID 644 649 BY SIMILARITY.
FT METAL 79 79 IRON 1.
FT METAL 111 111 IRON 1.
FT METAL 211 211 IRON 1.

FT	METAL	272	272	IRON 1.
FT	METAL	414	414	IRON 2.
FT	METAL	452	452	IRON 2.
FT	METAL	545	545	IRON 2.
FT	METAL	614	614	IRON 2.
FT	BINDING	136	136	CARBONATE 1.
FT	BINDING	140	140	CARBONATE 1.
FT	BINDING	142	142	CARBONATE 1.
FT	BINDING	143	143	CARBONATE 1.
FT	BINDING	143	143	CARBONATE 1.
FT	BINDING	478	478	CARBONATE 2.
FT	BINDING	482	482	CARBONATE 2.
FT	BINDING	484	484	CARBONATE 2.
FT	BINDING	485	485	CARBONATE 2.
FT	CARBOHYD	252	252	CARBONATE 2.
FT	CARBOHYD	387	387	CARBONATE 2.
FT	CARBOHYD	495	495	CARBONATE 2.
FT	CARBOHYD	564	564	CARBONATE 2.
FT	CONFLICT	63	63	RA -> A (IN REF. 4).
FT	CONFLICT	66	67	RA -> V (IN REF. 2).
FT	CONFLICT	145	145	I -> V (IN REF. 1 AND 4).
FT	CONFLICT	164	165	LQ -> PE (IN REF. 1).
FT	CONFLICT	264	264	C -> Y (IN REF. 4).
FT	CONFLICT	273	273	A -> P (IN REF. 4).
FT	CONFLICT	281	281	G -> A (IN REF. 4).
FT	CONFLICT	291	291	S -> R (IN REF. 4).
FT	CONFLICT	297	297	F -> S (IN REF. 2).
FT	CONFLICT	340	340	G -> A (IN REF. 4).
FT	CONFLICT	418	418	I -> V (IN REF. 1).
FT	CONFLICT	439	439	H -> Y (IN REF. 4).
FT	CONFLICT	459	459	K -> R (IN REF. 4).
FT	CONFLICT	514	514	A -> R (IN REF. 1).
FT	CONFLICT	632	632	H -> R (IN REF. 5).
FT	STRAND	25	26	/FTID-CAR 000198.
FT	HELIX	32	45	E -> A (IN REF. 4).
FT	HELIX	46	48	RA -> PG (IN REF. 2).
FT	STRAND	53	57	I -> V (IN REF. 1 AND 4).
FT	HELIX	61	69	LQ -> PE (IN REF. 1).
FT	TURN	70	71	C -> Y (IN REF. 4).
FT	STRAND	75	78	A -> P (IN REF. 4).
FT	HELIX	80	87	G -> A (IN REF. 4).
FT	TURN	89	91	S -> R (IN REF. 4).
FT	STRAND	93	102	F -> S (IN REF. 2).
FT	STRAND	107	108	G -> A (IN REF. 4).
FT	STRAND	110	118	I -> V (IN REF. 1).
FT	TURN	126	127	H -> Y (IN REF. 4).
FT	TURN	129	130	K -> R (IN REF. 4).
FT	STRAND	133	135	A -> R (IN REF. 1).
FT	TURN	138	139	H -> R (IN REF. 5).
FT	TURN	141	144	/FTID-CAR 000198.
FT	HELIX	145	155	E -> A (IN REF. 4).
FT	TURN	156	156	RA -> PG (IN REF. 2).
FT	TURN	159	161	I -> V (IN REF. 1 AND 4).
FT	HELIX	164	169	LQ -> PE (IN REF. 1).
FT	TURN	170	171	C -> Y (IN REF. 4).
FT	STRAND	175	176	A -> P (IN REF. 4).
FT	TURN	178	179	G -> A (IN REF. 4).
FT	TURN	182	184	S -> R (IN REF. 4).
FT	HELIX	186	188	F -> S (IN REF. 2).
FT	TURN	190	191	G -> A (IN REF. 4).
FT	TURN	196	197	I -> V (IN REF. 1).

Query Match 50.2%; Score 134; DB 1; Length 708;
Best Local Similarity 43.5%; Pred. No. 1.3e-09;
Matches 20; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
Oy 3 RRSYQWCAVSQPEATKCFQWQRMKRGVPGVCIKSDSIQICIA 48
Db 22 RKNVWCTTISQPEWFKCRWQMKLGAISITCVRAAFALCIRA 67

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RESULT 8
ICA_PIG STANDARD; PRT; 704 AA.
AC Q29545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inhibitor of carbonic anhydrase precursor.
GN ICA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97254619; PubMed=9100029;
RA "Weinberg M.W., Roush E.D., Decastro C.M., Fierke C.A.;
RT "Cloning, sequencing, and recombinant expression of the porcine
RT inhibitor of carbonic anhydrase: a novel member of the transferrin
RT family.";
RL Biochemistry 36:4327-4336(1997).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93099129; PubMed=1463741;
RA Roush E.D., Fierke C.A.;
RT "Purification and characterization of a carbonic anhydrase II
RT inhibitor from porcine plasma.";
RL Biochemistry 31:12536-12542(1992).
CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
CC with nonomolar affinity.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U36916; AAB58956.1; -.
DR PIR; I47228; I47228.
DR HSSP; P19134; 1TFD.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 704
FT CARBOHYD 491 491
SQ SEQUENCE 704 AA; 77634 MW; 16B0B651931E36 CRC64;

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Query Match 49.6%; Score 132.5; DB 1; Length 704;
Best Local Similarity 49.0%; Pred. No. 2e-09;
Matches 24; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

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QY 3 RRSVQNCVNSQPEATKCFQWQRMNRK--VRGPFVSCIRDPFIQIQIA 48
Db 22 KETVPMCTVSSQASKSCSFRRNMKILLFVEGPHVSCVXRSTYLCIRA 70

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RESULT 9
TRFE_PIG STANDARD; PRT; 696 AA.
AC P09571;

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DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sero-transferrin (transferrin) (Siderophilin) (beta-1-metal binding
DE globulin).
GN TF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88335629; PubMed=3419934;
RA Baldwin G.S., Weinstein J.;
RT "Nucleotide sequence of porcine liver transferrin.";
RL Nucleic Acids Res. 16:8720-8720(1988).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X12386; CA30943.1; -.
DR PIR; S01384; S01384.
DR PDB; 1H76; 15-JAN-02.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW 3D-structure.
FT REPEAT 1 340
FT REPEAT 341 696
FT DISULFID 9 47
FT DISULFID 19 38
FT DISULFID 117 198
FT DISULFID 157 173
FT DISULFID 160 181
FT DISULFID 170 183
FT DISULFID 231 245
FT DISULFID 343 305
FT DISULFID 349 381
FT DISULFID 359 372
FT DISULFID 406 682
FT DISULFID 423 646
FT DISULFID 456 532
FT DISULFID 480 673
FT DISULFID 490 504
FT DISULFID 501 515
FT DISULFID 572 586
FT DISULFID 624 629
FT METAL 62
FT METAL 94
FT METAL 192
FT METAL 253

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FT METAL 396 396 IRON 2 (BY SIMILARITY).
FT METAL 431 431 IRON 2 (BY SIMILARITY).
FT METAL 526 526 IRON 2 (BY SIMILARITY).
FT METAL 594 594 IRON 2 (BY SIMILARITY).
FT BINDING 119 119 CARBONATE 1 (BY SIMILARITY).
FT BINDING 123 123 CARBONATE 1 (BY SIMILARITY).
FT BINDING 125 125 CARBONATE 1 (BY SIMILARITY).
FT BINDING 126 126 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 126 126 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 458 458 CARBONATE 2 (BY SIMILARITY).
FT BINDING 462 462 CARBONATE 2 (BY SIMILARITY).
FT BINDING 464 464 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT BINDING 465 465 CARBONATE 2 (VIA AMIDE NITROGEN) (BY
SIMILARITY).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 497 497 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 308 308 K -> R.
SQ SEQUENCE 696 AA; 76967 MM; 787059F42D844B26 CRC64;

Query Match 44.9%; Score 120; DB 1; Length 696;
Best Local Similarity 43.8%; Pred. No. 8e-08;
Matches 21; Conservative 11; Mismatches 14; Indels 2; Gaps 1;

QY 3 RESVOMCAVSQPEATKCFQMQRMRKV--RGPPVSGTKRSPICQIOA 48
Db 3 QKIVKCTISNQANCKSSFRKNSKAVKNGPLVSCVKSSYDCTKA 50

RESULT 10
TREE HUMAN STANDARD; PRT; 698 AA.
ID _TREE HUMAN STANDARD; PRT; 698 AA.
AC P02757; O43890; Q9NOB8; Q9UHY0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
binding globulin) (PRO1400).
GN TF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*D1.
RX MEDLINE=84194084; PubMed=65985825;
RA Yang P., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
van Bragt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal
localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832;
RA Schaeffer E., Lucero M.A., Veltsch J.-M., Py M.-C., Levin M.J.,
Chamoun P., Cohen G.N., Zakin M.M.;
RT "Complete structure of the human transferrin gene. Comparison with
analogous chicken gene and human pseudogene.";
RL Gene 56:109-116 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
MEDLINE=9221399; PubMed=1809186;
RA Herisberger C.L., Larson J.L., Arnold B., Roelck P.R. Jr.,
Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W.,
Tice P.A.;
RT "A cloned gene for human transferrin";
RL Ann. N.Y. Acad. Sci. 646:140-154 (1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
FAitbanks V.F.;
RT "Molecular characterization of a case of atransferrinemia.";
RL Blood 96:4071-4074 (2000).
RN [5]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
by analysis of cDNA clones from human fetal liver";
RN [6]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frahn M., Park I., Beaumont C., Maessen G., Trepac J.S.,
Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
transferrin.";
RL Biochem. Biophys. Res. Commun. 119:273-281 (1984).
RN [7]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
Linbeck-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
seven cyanogen bromide fragments and the assembly of the complete
structure.";
RL J. Biol. Chem. 258:3543-3553 (1983).
RN [8]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
originated by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153 (1985).
RN [9]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=8706744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
regulatory sites.";
RL Nucleic Acids Res. 14:8692-8692 (1986).
RN [10]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
which match the control elements regulated by heavy metals,
glucocorticoids and acute phase reaction.";
RL Gene 49:167-175 (1986).
RN [11]
RP SEQUENCE OF 45-72 FROM N.A.
RX MEDLINE=20392111; PubMed=10931525;
RA de Ariba Zeira G.A., Salen M.-C., Fernandez P.M., Guillou F.,
Espinoza de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
differentiation of a human oligodendrocyte cell line.";
RL J. Neurosci. Res. 61:388-395 (2000).
RN [12]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF*C2.
RC TISSUE=Brain;
MEDLINE=97418135; PubMed=9272172;
RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (TF): a single mutation at codon 570 determines TF
C1 or TF C2 variant.";
RL Hum. Genet. 100:457-458 (1997).
RN [13]
RP SEQUENCE OF 564-624 FROM N.A.
RX Tsuchida S., Ikemoto S., Kajii E.;
RA Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE OF 636-696 FROM N.A.
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RX MEDLINE=89386721; PubMed=2780570;
 RA "Duguid J.R., Belmont C.W., Liu N.G., Tourtellotte W.W.;
 RT "Changes in brain gene expression shared by scrapie and Alzheimer
 RT disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
 RN [15]
 RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyova M.A., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Ershova E.S., Egorov T.A., Musalyanov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [16]
 RP DISULFIDE BONDS.
 RX MEDLINE=82222166; PubMed=6953407;
 RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.;
 RT "The complete amino acid sequence of human serum transferrin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
 RN [17]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
 RT "Expression and initial characterization of five site-directed
 RT mutants of the N-terminal half-molecule of human transferrin.";
 RL Biochemistry 30:10824-10829(1991).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
 RX MEDLINE=98272665; PubMed=9609685;
 RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.;
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.";
 RL Biochemistry 37:7919-7928(1998).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
 RX MEDLINE=98434369; PubMed=9760232;
 RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
 RA Woodworth R.C., Baker E.N.;
 RT "Rigand-induced conformational change in transferrins: crystal
 RT structure of the open form of the N-terminal half-molecule of human
 RT transferrin.";
 RL Biochemistry 37:13978-13986(1998).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
 RX MEDLINE=99155227; PubMed=10029548;
 RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
 RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.;
 RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe
 RT of human transferrin expressed in *Pichia pastoris* is folded correctly
 RT but is glycosylated on serine-32.";
 RL Biochemistry 38:2535-2541(1999).
 RN [21]
 RP VARIANT SER-142.
 RX MEDLINE=98019079; PubMed=9358047;
 RA Evans P., Kemp J.;
 RT "Exon/intron structure of the human transferrin receptor gene.";
 RL Gene 199:123-131(1997).
 RN [22]
 RP VARIANT GLU-646.
 RX MEDLINE=99020112; PubMed=9803271;
 RA Pang H., Koda Y., Soejima M., Kimura H.;
 RT "Identification of a mutation (A1879G) of transferrin from cDNA
 RT prepared from peripheral blood cells.";
 RL Ann. Hum. Genet. 62:271-274(1998).
 RN [23]
 RP VARIANTS SER-277; SER-589 AND GLU-671, AND CHARACTERIZATION OF
 RP VARIANT SER-277
 RX MEDLINE=21560266; PubMed=11703331;

RA Lee P.L., Halloran C., Trevino R., Felitti V., Beutler E.;
 RT "Human transferrin G277S mutation: a risk factor for iron deficiency
 RT anaemia.";
 RL Br. J. Haematol. 115:329-333(2001).
 RN [24]
 RP VARIANTS SER-277 AND SER-589
 RX MEDLINE=21558434; PubMed=11702220;
 RA Douabin-Gicquel V., Soriano N., Ferran H., Wojcik F., Palierne E.,
 RA Tami S., Jovein T., McKie A.T., Le Gall J.-Y., David V., Mosser J.;
 RT "Identification of 96 single nucleotide polymorphisms in eight genes
 RT involved in iron metabolism: efficiency of bioinformatic extraction
 RT compared with a systematic sequencing approach.";
 RL Hum. Genet. 109:393-401(2001).
 CC
 Query Match 44.4%; Score 118.5; DB 1; Length 698;
 Best Local Similarity 45.8%; Pred. No. 1.3e-07;
 Matches 22; Conservative 13; Mismatches 10; Indels 3; Gaps 1;
 Oy 4 RSVQWCAVSGPEATKCFQWQNRKX---RGPVSCIKRDSPIQIOA 48
 Db 23 KIVRWCAVSEHATKCSFDRHKSIVPSGFSVACVKSAYDCIRA 70
 CC
 RESULT 11
 TRFL.PIG STANDARD; PRT; 704 AA.
 AC P16632; Q29557;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin).
 GN LTF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid:9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92379101; PubMed=1511016;
 RA Lyndon J.P., O'Valley B.R., Saucedo O., Lee T., Haddon D.R.,
 RA Connely O.W.;
 RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
 RL Biochim. Biophys. Acta 1132:97-99(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92367939; PubMed=1503259;
 RA Alexander L.J., Levine M.B., Teng C.T., Beattie C.W.;
 RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
 RL Ann. Genet. 23:251-256(1992).
 RN [3]
 RP SEQUENCE OF 20-49.
 RX MEDLINE=9010538; PubMed=2605266;
 RA Hurchens T.W., Magnuson J.S., Yip T.-T.;
 RT "Rapid purification of porcine colostral whey lactoferrin by affinity
 RT chromatography on single-stranded DNA-agarose. Characterization,
 RT amino acid composition and N-terminal amino acid sequence.";
 RL Biochim. Biophys. Acta 999:323-329(1989).
 CC -1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
 CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
 CC OF AN ANION, USUALLY BICARBONATE.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC
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FT DISULFID 441 663 BY SIMILARITY.
FT DISULFID 473 549 BY SIMILARITY.
FT DISULFID 497 690 BY SIMILARITY.
FT DISULFID 507 521 BY SIMILARITY.
FT DISULFID 518 532 BY SIMILARITY.
FT DISULFID 569 603 BY SIMILARITY.
FT DISULFID 641 646 BY SIMILARITY.
FT METAL 81 81 IRON 1 (BY SIMILARITY).
FT METAL 113 113 IRON 1 (BY SIMILARITY).
FT METAL 211 211 IRON 1 (BY SIMILARITY).
FT METAL 272 272 IRON 1 (BY SIMILARITY).
FT METAL 414 414 IRON 2 (BY SIMILARITY).
FT METAL 449 449 IRON 2 (BY SIMILARITY).
FT METAL 543 543 IRON 2 (BY SIMILARITY).
FT METAL 611 611 IRON 2 (BY SIMILARITY).
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FT BINDING 144 144 CARBONATE 1 (BY SIMILARITY).
FT BINDING 145 145 CARBONATE 1 (BY SIMILARITY).
FT BINDING 145 145 CARBONATE 2 (BY SIMILARITY).
FT BINDING 475 475 CARBONATE 2 (BY SIMILARITY).
FT BINDING 479 479 CARBONATE 2 (BY SIMILARITY).
FT BINDING 481 481 CARBONATE 2 (BY SIMILARITY).
FT BINDING 482 482 CARBONATE 2 (BY SIMILARITY).
FT BINDING 514 514 CARBONATE 2 (BY SIMILARITY).
FT CARBOHYD 704 AA, 77753 MM, D87B2AFB46C708D CR664;
SQ SEQUENCE

Query Match 41.9%; Score 112; DB 1; Length 704;
Best Local Similarity 42.6%; Pred. No. 8.6e-07;
Matches 20; Conservative 12; Mismatches 13; Indels 2; Gaps 1;

Cy 4 RSVQKAVSOPETKCFQRMNRKV--RGPPSCIKRSPQICQIA 48
Db 23 RTVRCWCTISTHANKKASFRENVRLTESGPFVSCYKXSHMDCLKA 69

RESULT 13
TREE-RABIT STANDARD; PRT; 695 AA.
ID P19134; 046514;
AC 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN TP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91274362; PubMed=2054387;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umeias T.M.,
RA Woodworth R.C., Macgillivray R.T.A.;
RT "The nucleotide sequence of rabbit liver transferrin cDNA.";
RL Biochim. Biophys. Acta 1089:262-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Chareeb B.A.A., Thepot D., Pissant C., Cajero-Duarez M.,
RA Houdebine L.M.;
RT "Cloning and structural organisation of the rabbit transferrin encoding
RT gene.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 20-51.
RX MEDLINE=88209278; PubMed=3365331;
RA Godovac-Zimmermann J.;

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RT "Isolation, characterization and N-terminal amino-acid sequence of
RT rabbit transferrin.";
RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN [4]
RP SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=3169252;
RA Evans R.W., Aitken A., Patel K.J.;
RT "Evidence for a single glycan moiety in rabbit serum transferrin and
RT location of the glycan within the polypeptide chain.";
RL FEBS Lett. 238:39-42(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=1179277;
RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
RA Horsburgh C., Uchil H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sarra R., Garratt R.C., Gorinsky B., Uchil H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin:
RT preliminary structure analysis of the N-terminal half-molecule at
RT 2.3-A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X58533; CA441424.1; -
DR EMBL; AF031625; AAB94136.1; JOINED.
DR EMBL; AF031611; AAB94136.1; JOINED.
DR EMBL; AF031612; AAB94136.1; JOINED.
DR EMBL; AF031613; AAB94136.1; JOINED.
DR EMBL; AF031614; AAB94136.1; JOINED.
DR EMBL; AF031615; AAB94136.1; JOINED.
DR EMBL; AF031616; AAB94136.1; JOINED.
DR EMBL; AF031617; AAB94136.1; JOINED.
DR EMBL; AF031618; AAB94136.1; JOINED.
DR EMBL; AF031619; AAB94136.1; JOINED.
DR EMBL; AF031620; AAB94136.1; JOINED.
DR EMBL; AF031621; AAB94136.1; JOINED.
DR EMBL; AF031622; AAB94136.1; JOINED.
DR EMBL; AF031623; AAB94136.1; JOINED.
DR EMBL; AF031624; AAB94136.1; JOINED.
DR PDB; 1TFD; 15-APR-93.
DR PDB; 1JNF; 09-JAN-02.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin.
DR PRINTS; PRO0422; TRANSFERRIN.
DR SMART; SM00094; TR_PFR; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
KW Signal; 3D-structure.
FT SIGNAL 1 19

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FT REPEAT 20 355
FT REPEAT 356 695
FT DISULFID 28 67
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FT DISULFID 579 593
FT DISULFID 631 636
FT CARBOHYD 509 509
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
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FT METAL 533 533
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FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 91 94
FT STRAND 96 102
FT STRAND 114 121
FT TURN 122 123
FT TURN 128 129
FT TURN 132 133
FT STRAND 136 137
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT TURN 155 157
FT HELIX 155 170
FT TURN 171 172
FT STRAND 176 177
FT TURN 179 180
FT STRAND 190 195
FT TURN 194 195
FT HELIX 207 214
FT TURN 215 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 228 232

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SEROTRANSFERRIN.

1.
2.

N-LINKED (GLCNAC. .).

IRON 1.
IRON 1.
IRON 1.
IRON 1.
IRON 2.
IRON 2.
IRON 2.
CARBONATE 1.
CARBONATE 1.
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 1 (VIA AMIDE NITROGEN).
CARBONATE 2.
CARBONATE 2.
CARBONATE 2 (VIA AMIDE NITROGEN).
CARBONATE 2 (VIA AMIDE NITROGEN).
V -> I.
MISSING (IN REF. 1).
K -> S (IN REF. 3).
P -> Y (IN REF. 3).

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FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 246
FT TURN 247 249
FT STRAND 250 253
FT TURN 254 255
FT TURN 257 259
FT STRAND 263 265
FT STRAND 269 273
FT HELIX 279 288
FT TURN 289 291
FT TURN 303 304
FT STRAND 306 306
FT TURN 307 308
FT STRAND 309 309
FT TURN 316 317
FT STRAND 321 322
SQ SEQUENCE 695 AA; 76670 MW; DB12F34D87AE9D55 CRC64;

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Query Match 41.4%; Score 110.5; DB 1; Length 695;
Best Local Similarity 41.7%; Pred. No. 1.3e-06;
Matches 20; Conservative 14; Mismatches 11; Indels 3; Gaps 1;

Qy 4 RSVQCAVSOPEATKCFQCHMRKV--RGPVSCIKEDSPIQIOA 48
Db 23 KTVKCAVNDHDSKCANFRDSMKVLPEDGPRIICVKKASYLDICIX 70

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RESULT 14
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AC Q921I1; Q5421; Q61803; Q62358; Q62359; Q63915; Q64515; Q8VII5;
AC Q922C0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-FAR-2004 (Rel. 43, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Beta-1-metal
binding globulin).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Lai D.-Z.;
RT "Construction of a robust CHO cell-line for biopharmaceutical
production.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22386357; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Canninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 1-11 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=98284323; PubMed=6621303;
 RA Chaudhary J., Skinner M.K.;
 RT "Comparative sequence analysis of the mouse and human transferrin
 RT promoters: hormonal regulation of the transferrin promoter in Sertoli
 RT cells";
 RL Mol. Reprod. Dev. 50:273-283(1998).
 RN [4]
 RP SEQUENCE OF 277-337; 462-496 AND 526-575 FROM N.A.
 RX MEDLINE=8086992; PubMed=3693348;
 RA Chen L.-H., Bissell M.J.;
 RT "Transferrin mRNA level in the mouse mammary gland is regulated by
 RT pregnancy and extracellular matrix";
 RL J. Biol. Chem. 262:17247-17250(1987).
 RN [5]
 RP SEQUENCE OF 268-307 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94068311; PubMed=8248032;
 RA Kasik J.W., Rice E.J.;
 RT "Transferrin gene expression in maternal liver, fetal liver and
 RT placenta during pregnancy in the mouse";
 RL Placenta 14:365-371(1993).
 RN [6]
 RP SEQUENCE OF 282-412 FROM N.A.
 RX MEDLINE=87280033; PubMed=3611056;
 RA Pentecost B.T., Teng C.T.;
 RT "Lactotransferrin is the major estrogen inducible protein of mouse
 RT uterine secretions";
 RL J. Biol. Chem. 262:10134-10139(1987).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation
 CC to those of storage and utilization. Serum transferrin may also
 CC have a further role in stimulating cell proliferation.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
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 DR EMBL: AF440692; AAI34533.1; -;
 DR EMBL: BC012313; AAH12313.1; -;
 DR EMBL: BC022986; AAH22986.1; -;
 DR EMBL: BC008559; AAH08559.1; -;
 DR EMBL: AF027336; AAB84034.1; -;
 DR EMBL: M23015; AAA40499.1; -;
 DR EMBL: M23015; AAA40499.1; -;
 DR EMBL: M23016; AAA40491.1; -;
 DR EMBL: S67217; AAB28966.2; -;
 DR EMBL: J03299; AAA39438.1; -;
 DR PIR: A28446; A28446;
 DR MGD: MGI:98821; Trf.
 DR GO: GO:0030139; Cyendocytic vesicle; IDA.
 DR InterPro: IPR001156; Transferrin.
 DR Pfam: Pf00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR PROSITE: PS00205; TRANSFERRIN 1; 1.
 DR PROSITE: PS00206; TRANSFERRIN 2; 2.
 DR PROSITE: PS00207; TRANSFERRIN 3; 2.
 KM Transports; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KM Signal.

FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 697 SEROTRANSFERRIN.
 FT REPEAT 20 355 1.
 FT REPEAT 356 697 2.
 FT DISULFID 28 67 BY SIMILARITY.
 FT DISULFID 38 58 BY SIMILARITY.
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 FT BINDING 143 143 CARBONATE 1 (BY SIMILARITY).
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 FT SIMILARITY).
 FT BINDING 146 146 CARBONATE 1 (VIA AMIDE NITROGEN) (BY
 FT SIMILARITY).
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 FT BINDING 478 478 CARBONATE 2 (BY SIMILARITY).
 FT BINDING 480 480 CARBONATE 2 (VIA AMIDE NITROGEN)
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 FT CONFLICT 71 74 ISAS -> HASG (IN REF. 2; AAH08559).
 FT CONFLICT 283 283 W -> L (IN REF. 5).
 FT CONFLICT 307 307 P -> L (IN REF. 5).
 FT CONFLICT 350 351 CP -> SA (IN REF. 6).
 FT CONFLICT 487 487 G -> C (IN REF. 4).
 FT CONFLICT 527 527 A -> D (IN REF. 4).
 FT CONFLICT 575 575 K -> N (IN REF. 4).
 FT CONFLICT 697 697 H -> S (IN REF. 1).
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 Query Match 39.98; Score 106.5; DB 1; Length 697;
 Best local Similarity 41.78; Pred. No. 4.3e-06;
 Matches 20; Conservative 13; Mismatches 12; Indels 3; Gaps 1;
 Cx 4 RSYVQWASVSOPEATKCFOWORNNRKY---RGPPVSCIKRSDPIQIOA 48
 Db 23 KTVKMCVASEHENTKCSIFPDHAKTVLPDGPRLACVCKKSYDCLTKA 70
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 TRFE RAT STANDARD: PRT; 698 AA.
 AC P12316; O64628; O64630;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 15-OCT-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
 DE binding globulin).
 GN TF.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=96208933; PubMed=8829802;
 RA Hosino A., Hisayasu S., Shimada T.;
 RT "Complete sequence analysis of rat transferrin and expression of
 transferrin but not lactoferrin in the digestive glands.";
 RL Comp. Biochem. Physiol. 113B:491-497(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Mammary gland;
 RX MEDLINE=95234054; PubMed=7717992;
 RA Escriva H., Pierce A., Coddeville B., Gonzalez F., Benaisa M.,
 RA Leger D., Wieruszkei J.M., Spik G., Pambianco M.;
 RT "Rat mammary-gland transferrin: nucleotide sequence, phylogenetic
 analysis and glycan structure.";
 RL Biochem. J. 307:47-55(1995).
 RN [3]
 RP SEQUENCE OF 20-47.
 RX MEDLINE=80049855; PubMed=500689;
 RA Schreiber G., Dryburgh H., Miliership A., Matsuda Y., Inglis A.,
 RA Phillips J., Edwards K., Maggs J.;
 RT "The synthesis and secretion of rat transferrin.";
 RL J. Biol. Chem. 254:12013-12019(1979).
 RN [4]
 RP SEQUENCE OF 521-698 FROM N.A.
 RX MEDLINE=87056339; PubMed=3023031;
 RA Hugueny J.I., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
 RA Grissold M.D.;
 RT "Transferrin messenger ribonucleic acid: molecular cloning and
 hormonal regulation in rat Sertoli cells.";
 RL Endocrinology 120:332-340(1987).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 can bind two atoms of ferric iron in association with the binding
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 transport of iron from sites of absorption and heme degradation to
 those of storage and utilization. Serum transferrin may also have
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 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D38380; BAA07458.1; -
 DR EMBL: X77158; CAA54403.1; -
 DR EMBL: M27966; AAA42267.1; -
 DR PIR: S49163; S49163.
 DR HSSP: P19134; ITFD.
 DR GlycosultedB; P12346; -
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 DR Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
 KM Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 698 SEROTRANSFERRIN.
 FT REPEAT 20 355 1.

FT	REPEAT	356	698	2.
FT	DISULFID	28	67	BY SIMILARITY.
FT	DISULFID	38	58	BY SIMILARITY.
FT	DISULFID	137	213	BY SIMILARITY.
FT	DISULFID	156	350	BY SIMILARITY.
FT	DISULFID	177	193	BY SIMILARITY.
FT	DISULFID	180	196	BY SIMILARITY.
FT	DISULFID	190	198	BY SIMILARITY.
FT	DISULFID	246	260	BY SIMILARITY.
FT	DISULFID	363	395	BY SIMILARITY.
FT	DISULFID	373	386	BY SIMILARITY.
FT	DISULFID	420	693	BY SIMILARITY.
FT	DISULFID	435	656	BY SIMILARITY.
FT	DISULFID	471	542	BY SIMILARITY.
FT	DISULFID	495	684	BY SIMILARITY.
FT	DISULFID	505	519	BY SIMILARITY.
FT	DISULFID	516	525	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	634	639	BY SIMILARITY.
FT	METAL	82	82	IRON 1 (BY SIMILARITY).
FT	METAL	114	114	IRON 1 (BY SIMILARITY).
FT	METAL	207	207	IRON 1 (BY SIMILARITY).
FT	METAL	268	268	IRON 1 (BY SIMILARITY).
FT	METAL	410	410	IRON 2 (BY SIMILARITY).
FT	METAL	447	447	IRON 2 (BY SIMILARITY).
FT	METAL	536	536	IRON 2 (BY SIMILARITY).
FT	METAL	604	604	IRON 2 (BY SIMILARITY).
FT	BINDING	139	139	CARBONATE 1 (BY SIMILARITY).
FT	BINDING	143	143	CARBONATE 1 (BY SIMILARITY).
FT	BINDING	145	145	CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	146	146	CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	473	473	CARBONATE 2 (BY SIMILARITY).
FT	BINDING	477	477	CARBONATE 2 (BY SIMILARITY).
FT	BINDING	479	479	CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	BINDING	480	480	CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).
FT	CARBOHD	512	512	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	57	57	A -> P (IN REF. 2).
FT	CONFLICT	110	110	P -> R (IN REF. 2).
FT	CONFLICT	318	354	AFGCGVPPRDYRLVGHSVYTAIRNQGECVEAS -> RFGLRAPKDELQAVPRPOLCHSKSKAGSCPDA (IN REF. 2).
FT	CONFLICT	380	380	S -> G (IN REF. 2).
FT	CONFLICT	691	691	E -> D (IN REF. 4).
FT	CONFLICT	696	697	HK -> TA (IN REF. 4).
FT	SEQUENCE	698 AA;	76363 MW;	DDF2C1918E2A1B08 CXC64;

Query Match 39.9%; Score 106.5; DB 1; Length 698;
 Best Local Similarity 41.7%; Pred. No. 4.3e-06;
 Matches 20; Conservative 13; Mismatches 12; Indels 3; Gaps 1;

Qy 4 RSVQCAVSPQPAIKCFQGMNRKV--RGPVSCIKRDSPIQIOA 48
 Db 23 KTVKCAVSEHENTKICISFRDMKTVLPADGPRLACVAKTSYQDCICA 70

Search completed: September 1, 2004, 00:10:44
 UDS time : 17.4867 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:56:54 ; Search time 88.96 Seconds
(without alignments)
170.244 Million cell updates/sec

Title: US-09-508-095-19

Sequence: 1 GRRSYQWCAVSGPEATKCF.....VRGPPVSCIKRDSPIQICQA 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_rhbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	97.8	234	4	Q8IX02
2	254	95.1	711	4	Q8IZ86
3	254	95.1	711	4	Q8IU92
4	253	94.8	711	4	Q8TCD2
5	163	61.0	707	11	Q8CBA0
6	144.5	54.1	38	4	Q9UCY5
7	120	44.2	704	6	Q8MNM8
8	118	44.2	704	6	Q7YS20
9	115	43.1	333	6	Q9TR80
10	112.5	42.1	700	11	Q9DBD0
11	109.5	41.0	694	11	Q7TSX8
12	106.5	39.9	698	11	Q7TNX0
13	106.5	39.9	700	11	Q8VC96
14	106.5	39.9	979	11	Q7TMC7
15	106.5	39.9	980	11	Q7TMC7
16	103	38.6	54	6	Q9TQV7

17	101	37.8	711	6	Q9XT72
18	92.5	34.6	87	11	Q63602
19	92	34.5	421	11	Q7TP83
20	86.5	32.4	691	13	Q9PT13
21	85.5	32.0	517	13	Q8TUK7
22	85.5	32.0	672	13	Q9PU08
23	83.5	31.3	382	13	Q9DFK6
24	82.5	30.9	677	13	Q9I8R0
25	82.5	30.9	677	13	Q9PT58
26	82.5	30.9	677	13	Q9I866
27	81.5	30.5	676	13	Q9I8R2
28	81.5	30.5	677	13	Q9PT53
29	81.5	30.5	677	13	Q9PT55
30	81.5	30.5	677	13	Q9I8R3
31	81.5	30.5	677	13	Q9I887
32	80.5	30.1	367	13	Q9I8F7
33	79.5	29.8	691	13	Q9PU70
34	79.5	29.8	691	13	Q7TI93
35	78.5	29.4	72	13	Q8AUN8
36	78.5	29.4	691	13	Q9PU66
37	77.5	29.0	691	13	Q9PRH5
38	77.5	29.0	691	13	Q9PU67
39	76.5	28.7	71	13	Q8AUP0
40	76.5	28.7	672	13	Q9PT57
41	76.5	28.7	677	13	Q9I858
42	76.5	28.7	677	13	Q9I809
43	76.5	28.7	691	13	Q9PU68
44	76	28.5	686	13	Q9I882
45	75.5	28.3	71	13	Q8AUG2

ALIGNMENTS

RESULT 1

Q8IX02

PRELIMINARY;

PRT; 234 AA.

AC Q8IX02:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Lactoferrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Li N.,
RT "Human lactoferrin gene, 5' regulation region and exons 1-6.";
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF508798; AA014686.1; -.
DR GO; GO:0005576; C:cytoregulatory; IEA.
DR GO; GO:0008199; F:ferri iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PRR; 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
FT NON TER 234
FT 234
SQ SEQUENCE 234 AA; 25671 MW; 2A08DAFDB8B780C7 CRC64;

Query Match 97.8%; Score 261; DB 4; Length 234;

Best Local Similarity 100.0%; Pred. No. 2.1e-28; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRSYQWCAVSGPEATKCFQWGRNRRKVGPPVSCIKRDSPIQICQA 48
DB 22 RRRSYQWCAVSGPEATKCFQWGRNRRKVGPPVSCIKRDSPIQICQA 68

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RESULT 2
Q81ZB6 PRELIMINARY; PRT; 711 AA.
AC Q81ZB6;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Lactoferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kagiian J.B., Fine D.H.;
RT "Characterization of an amino acid polymorphism in the antibacterial
RT domain of human lactoferrin."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY137470; AN11304.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR01156; Transferrin.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
SQ SEQUENCE 711 AA; 78396 MW; 547AB9423C27CE67 CRC64;

Query Match 95.1%; Score 254; DB 4; Length 711;
Best Local Similarity 95.7%; Pred. No. 6.1e-27;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 2 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 48
Db 22 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 68

RESULT 3
Q81U92 PRELIMINARY; PRT; 711 AA.
AC Q81U92;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Lactoferrin precursor (Lactoferrin).
GN LTF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Singh T.P.;
RT "Homo sapiens lactoferrin gene: cDNA cloning and sequence
RT analysis."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=seminal vesicle;
RA Bakkar Singh S., Saravanan K., Paramasivam M., Srinivasan A.,
RA Singh T.P.;
RT "Homo sapiens lactoferrin (HLF) mRNA."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY165046; AAN63998.1; -
DR EMBL: AY178998; AAN75578.2; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.

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DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR01156; Transferrin.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 711 AA; 78382 MW; 547BFC42C9267867 CRC64;

Query Match 95.1%; Score 254; DB 4; Length 711;
Best Local Similarity 95.7%; Pred. No. 6.1e-27;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 2 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 48
Db 22 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 68

RESULT 4
Q8TCD2 PRELIMINARY; PRT; 711 AA.
AC Q8TCD2;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Lactoferrin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=prostate;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSFERRIN ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
DR EMBL: BC022347; AAH22347.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR01156; Transferrin.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Iron transport; Metal-binding; Transport.
SQ SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;

Query Match 94.8%; Score 253; DB 4; Length 711;
Best Local Similarity 97.9%; Pred. No. 8.4e-27;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 48
Db 22 RRRSVQWCAVSOPEATKCFQWQNMKRVGPPVSCIKRDSPIQICIA 68

RESULT 5
Q8CB40 PRELIMINARY; PRT; 707 AA.
AC Q8CB40;
ID Q8CB40;
OX Q8CB40;

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DT	01-MAR-2003	(TREMBLrel . 23 , Created)
DT	01-MAR-2003	(TREMBLrel . 23 , Last sequence update)
DT	01-OCT-2003	(TREMBLrel . 25 , Last annotation update)
DE	Lactoferrin.	
GN	LTF.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBJ_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Bone;	
RX	MEDLINE=22354683; PubMed=12466851;	
RA	The FANTOM Consortium,	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs."	
RL	Nature 420:563-573(2002)."	
EMBL	AK034651; BAC29450.1; ..	
DR	MGD; MGI:96837; Lef.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0008199; F:ferric iron binding; IEA.	
DR	GO; GO:0006879; P:piron ion homeostas; IEA.	
DR	GO; GO:0006826; P:piron ion transport; IEA.	
DR	InterPro; IPRO01156; Transferrin.	
DR	Pfam; PF00405; transferrin_2.	
DR	PRINTS; PR00422; TRANSFERRIN.	
DR	SMART; SMO0094; TR_FER; 2.	
DR	PROSITE; PS00205; TRANSFERRIN 1; 1.	
DR	PROSITE; PS00206; TRANSFERRIN 2; 2.	
DR	PROSITE; PS00207; TRANSFERRIN 3; 2.	
SQ	SEQUENCE 707 AA; 77837 MW; EI13ZP5FD8748A0F CRC64;	
Query Match	61.0%; Score 163; DB 11; Length 707;	
Best Local Similarity	63.6%; Pred.No.33e-14;	
Matches 28; Conservative 5; Mismatches 11; Indels 0; Gaps 0;		
Dd	5 SYQCWCAVSGPEATKCFOWQRNRKYRGVPVSCIRKDSPIIOCIQA 48 : : :: 23 TVQWCNVNSEBEKCLRMQNEKRXYGGPLSCVKKSSTROCIOA 66	
RESULT 6		
ID Q9UCYS	PRELIMINARY; PRT; 38 AA.	
AC Q9UCYS;		
DT 01-MAY-2000	(TREMBLrel . 13 , Created)	
DT 01-MAY-2000	(TREMBLrel . 13 , Last sequence update)	
DT 01-OCT-2003	(TREMBLrel . 25 , Last annotation update)	
OS Lactoferlin homolog (Fragment) .		
CS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX NCBI_TaxId=9606;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=96081613; PubMed=8551695;		
RA Sato I.		
RA "Characterization of the 84-kDa protein with ABH activity in human		
RT seminal plasma.";		
RL Jpn. J. Legal Med. 49:281-293(1995) .		
DR HSSP; O77811; IBIX.		
DR GO; GO:0005576; C:extracellular; IEA.		
DR GO; GO:0008199; F:ferric iron binding; IEA.		
DR GO; GO:0006879; P:piron ion homeostas; IEA.		
DR GO; GO:0006826; P:piron ion transport; IEA.		
DR InterPro; IPRO01156; Transferrin.		
DR Pfam; PF00405; transferrin_1.		
SQ SEQUENCE 38 AA; 4459 MW; 040ZF490B5BDDB CRC64;		

Qy	1	GR-FESVOMCAVSPQEARLKCSOMORNNRKYPGPVSCI	37
		1	GRFKXSVMQXAVSQPEADKXFCWQDNNRKYPGRPVSKH
Db	1	GRFKXSVMQXAVSQPEADKXFCWQDNNRKYPGRPVSKH	38
RESULT 7			
	Q8WMN8	PRELIMINARY;	PRT, 704 AA.
ID	Q8WMN8		
AC	Q8WMN8		
DT	01-MAR-2002 (T-EMBLrel. 1, 20, Created)		
DT	01-MAR-2002 (T-EMBLrel. 20, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Lactoferrin (Fragment).		
LN	LFE		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.		
OX	NCBI_TaxID=9823;		

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary Gland;
RA      Wang S.-R., Lin T.-Y., Wang C.-N.;
RL      "Isolation and expression of porcine milk lactoferrin."
CC      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases;
CC      - FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC      CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC      OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
CC      - SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
DR      EMBL, U77887; ALA0161.1; -;
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0008199; F:ferric iron binding; IEA.
DR      GO; GO:0006879; P:iron ion homeostasis; IEA.
DR      GO; GO:0006826; P:iron ion transport; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro: IPR001156; Transferrin.
DR      Pfam: PF00405; transferrin; 2.
DR      PRINTS: PR00422; TRANSFERRIN.
DR      SMART; SMO0094; TR_FER; 2.
DR      PROSITE; PS00205; TRANSFERRIN_1; 2.
DR      PROSITE; PS00206; TRANSFERRIN_2; 2.
DR      PROSITE; PS00207; TRANSFERRIN_3; 1.
KM      Glycoprotein; Iron transport; Metal-Binding; Transport.
FT      NON_TER
SQ      SEQUENCE 704 AA; 76661 MW; 64DE769F503CC32 CRC64;

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Query Match Similarity      44.9%; Score 120; DB 6; Length 704;
Best Local Similarity      43.5%; Pred. No. 3,4e-08;
Matches      20; Conservative      10; Mismatches      14; Indels      2; Gaps      1

Oy      3      RSVQWCAVSGPEATKCFQWQNNKRVGPPVSCIKRDSPIQICQ      48
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      22      KKGAVMCVISTAEYKCKRQWQSKIRTN--FIFCIRRASPFDCIRA      65

RESULT 8
Q7YS20
AC      Q7YS20      PRELIMINARY;      PRT;      704 AA.
DT      01-OCT-2003 (TREMBLrel. 25, Created)
DT      01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Lactoferrin.
GN      PLF.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
ON      (1)
RN      RP
RP      SEQUENCE FROM N.A.
RC      TISSUE=Mammary gland;
RA      Pecorini C., Fogher C., Baldi A.;
RT      "The nucleotide sequence of porcine lactoferrin cDNA."

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RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY306198; AAP70487.1;
 SQ SEQUENCE 704 AA; 77522 MW; AAC8E176756BFEA CRC64;

Query Match 44.8%; Score 118; DB 6; Length 704;
 Best Local Similarity 43.8%; Pred. No. 6, 5e-09;
 Matches 20; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

QY 3 RSVQWCAVSOPEATKCFQWQNRKVRGPPVSCIKRDSPIQICQ 48
 DB 22 KGVRCVISTAEYSKCRQWQSKIRRTN--PMFCIRASPTDCIRA 65

RESULT 9

Q9TR80 PRELIMINARY; PRT; 33 AA.

AC Q9TR80; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 ON NCBI_Taxid=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9512729; PubMed=7821104;
 RA Qian Z.Y., Jolles P., Migliore-Samou D., Fiat A.M.;
 RL Biochim. Biophys. Acta 1243:25-32(1995).
 DR PIR; S52107; S52107.
 DR HSP; 077698; ICE2.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferin.
 DR Pfam; PF00405; transferin; 1.
 SQ SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;

Query Match 43.1%; Score 115; DB 6; Length 33;
 Best Local Similarity 56.7%; Pred. No. 7, 7e-09;
 Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 3 RSVQWCAVSOPEATKCFQWQNRKVRGPP 32
 DB 3 RNVRCVISTAEYSKCRQWQSKIRRTN--PMFCIRASPTDCIRA 32

RESULT 10

Q9DBD0 PRELIMINARY; PRT; 700 AA.

AC Q9DBD0; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE 130001702Rik Protein.
 GN 130001702Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Agachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saeto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kacota K., Matsuda H.A., Ashburner N., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Bareh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK005035; BAB23762.1; -.
 DR HSP; P19134; ITPD.
 DR MGD; MGI:1919025; 130001702Rik.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferin.
 DR Pfam; PF00405; transferin; 2.
 DR PRINTS; PR00422; TRANSFERIN.
 DR SMART; SM00094; TR_PFR. 2.
 DR PROSITE; PS00205; TRANSFERIN_1; 1.
 DR PROSITE; PS00207; TRANSFERIN_3; 1.
 SQ SEQUENCE 700 AA; 76765 MW; 38C991D1021AE548 CRC64;

Query Match 42.1%; Score 112.5; DB 11; Length 700;
 Best Local Similarity 42.6%; Pred. No. 3, 8e-07;
 Matches 20; Conservative 13; Mismatches 11; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNRKVRGPPVSCIKRDSPIQICQ 47
 DB 23 KTRVRCVSDHEATKCSFRDNMKVLPAGGPAVTCVRKMSHPECIR 69

RESULT 11

Q7TSX8 PRELIMINARY; PRT; 694 AA.

AC Q7TSX8; 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Transferin.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 ON NCBI_Taxid=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Rinaudo J.A.S., Gerin J.L.;
 RT "Cross-species hybridization: Characterization of gene expression in
 RT woodchuck liver using human membrane arrays."
 RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY288100; AAP37129.1; -.
 SQ SEQUENCE 694 AA; 76466 MW; 40053F7D1CFC887 CRC64;

Query Match 41.0%; Score 109.5; DB 11; Length 694;
 Best Local Similarity 43.8%; Pred. No. 9, 9e-07;
 Matches 21; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNRKVRGPPVSCIKRDSPIQICQ 48
 DB 23 KTRVRCVSDHEATKCSFRDNMKVLPAGGPAVTCVRKMSHPECIR 70

RESULT 12

Q7TNX0 PRELIMINARY; PRT; 698 AA.

AC 07TNX0;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Liver regeneration-related protein LRK03.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RT "Liver regeneration after PH."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY327504; AAP97736.1; -;
 SQ SEQUENCE 698 AA; 76395 MW; B91AB841CA47194 CRC64;

Query Match 39.9%; Score 106.5; DB 11; Length 698;
 Best Local Similarity 41.7%; Pred. No. 2.6e-06;
 Matches 20; Conservative 13; Mismatches 12; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNNRKY--RGPPVSCIKRDSPIQICQA 48
 DB 23 KTVKWCASEHENTKCSIFRDHMKTVLPADGPRILACVKKTSYQDCIKR 70

RESULT 13
 ID 08VC96 PRELIMINARY; PRT; 700 AA.
 AC 08VC96;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RIKEN CDNA 130001J02 gene.
 GN 130001J02R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021390; AAH21390.1; -;
 DR MGD; MGI:119025; 130001J02R1K.
 DR GO; GO:0005576; C:cytoskeleton; IEA.
 DR GO; GO:0008199; F:cell-cell binding; IEA.
 DR GO; GO:0006826; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 SQ SEQUENCE 700 AA; 76795 MW; 7DA4A580CBB6B37 CRC64;

Query Match 39.9%; Score 106.5; DB 11; Length 700;
 Best Local Similarity 40.4%; Pred. No. 2.6e-06;
 Matches 19; Conservative 13; Mismatches 12; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNNRKY--RGPPVSCIKRDSPIQICQA 47
 DB 23 KTVKWCASEHENTKCSIFRDHMKTVLPADGPRILACVKKTSYQDCIKR 69

RESULT 14
 ID 07TMC7 PRELIMINARY; PRT; 979 AA.
 AC 07TMC7;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RIKEN CDNA 130001J02 gene.
 GN 130001J02R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021390; AAH21390.1; -;
 DR MGD; MGI:119025; 130001J02R1K.
 DR GO; GO:0005576; C:cytoskeleton; IEA.
 DR GO; GO:0008199; F:cell-cell binding; IEA.
 DR GO; GO:0006826; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00207; TRANSFERRIN_3; 1.
 SQ SEQUENCE 700 AA; 76795 MW; 7DA4A580CBB6B37 CRC64;

DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Ab2-417 (Cc1-8).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Chang C.F., Zhao L.F., Ma H., Wang L.,
 RA Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
 RA Yan H.M., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RT "Liver regeneration after PH."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY325214; AAP92615.1; -;
 DR EMBL; AY325214; AAP92615.1; -;
 SQ SEQUENCE 979 AA; 107411 MW; 5B80A6A1DD67D09 CRC64;

Query Match 39.9%; Score 106.5; DB 11; Length 979;
 Best Local Similarity 41.7%; Pred. No. 3.7e-06;
 Matches 20; Conservative 13; Mismatches 12; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNNRKY--RGPPVSCIKRDSPIQICQA 48
 DB 23 KTVKWCASEHENTKCSIFRDHMKTVLPADGPRILACVKKTSYQDCIKR 70

RESULT 15
 ID 07TP24 PRELIMINARY; PRT; 980 AA.
 AC 07TP24;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Bal-667.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
 RA Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RT "Liver regeneration after PH."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY355230; AAP92631.1; -;
 SQ SEQUENCE 980 AA; 107445 MW; 73B3AC3977E640FE CRC64;

Query Match 39.9%; Score 106.5; DB 11; Length 980;
 Best Local Similarity 41.7%; Pred. No. 3.7e-06;
 Matches 20; Conservative 13; Mismatches 12; Indels 3; Gaps 1;

QY 4 RSVQWCAVSOPEATKCFQWQNNRKY--RGPPVSCIKRDSPIQICQA 48
 DB 23 KTVKWCASEHENTKCSIFRDHMKTVLPADGPRILACVKKTSYQDCIKR 70

Search completed: September 1, 2004, 00:15:35
 Job time : 90.96 secs

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OM protein - protein search, using sw model

Run on: August 31, 2004, 23:54:24 ; Search time 28.88 Seconds
(without alignments)
117.402 Million cell updates/sec

Title: US-09-508-095-22
Perfect score: 60
Sequence: 1 AARARVMAAVG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	12	2	AAW93886 Bifidobac
2	56	93.3	12	2	AAW93878 Bifidobac
3	56	93.3	13	2	AAW93880 Bifidobac
4	56	93.3	687	2	AAW71183 Mutant hu
5	56	93.3	687	4	AAW77911 Human lac
6	56	93.3	688	2	AAW71182 Mutant hu
7	56	93.3	688	4	AAW77910 Human lac
8	56	93.3	689	4	AAW71181 Mutant hu
9	56	93.3	689	4	AAW77908 Human lac
10	56	93.3	690	2	AAW71180 Mutant hu
11	56	93.3	690	4	AAW77908 Human lac
12	56	93.3	690	5	ABG80724 Codon opt
13	56	93.3	690	5	AAE27884 Human cod
14	56	93.3	692	3	AAV58733 Human lac
15	56	93.3	692	4	AAW93882 Human lac
16	56	93.3	692	4	AAW77906 Human lac
17	56	93.3	692	5	AAE28002 Human cod
18	56	93.3	693	3	AAE85146 Lactoferr
19	56	93.3	705	2	AAW22423 Human lac
20	56	93.3	705	2	AAV31152 Human lac
21	56	93.3	708	2	AAW22424 Human lac
22	56	93.3	708	2	AAV31153 Human lac
23	56	93.3	709	2	AAW12583 Lactoferr
24	56	93.3	709	2	AAW45198 Human lac
25	56	93.3	709	2	AAW45199 Human lac

26	56	93.3	709	2	AAW21695 Human lac
27	56	93.3	709	2	AAW53879 Human lac
28	56	93.3	709	3	AAV77577 Human lac
29	56	93.3	709	3	AAW03830 Human lac
30	56	93.3	709	3	AAW36842 Protein e
31	56	93.3	709	7	AAE76659 Human lac
32	56	93.3	711	2	AAW08033 Human lac
33	56	93.3	711	2	AAW43653 Lactoferr
34	56	93.3	711	2	AAW09342 Human lac
35	56	93.3	711	2	AAW57317 Human lac
36	56	93.3	711	2	AAW53880 Bovine al
37	56	93.3	711	2	AAW86021 Human lac
38	56	93.3	711	3	AAV77578 Human lac
39	56	93.3	711	3	AAW03831 Human lac
40	56	93.3	711	3	AAW08182 Amino aci
41	56	93.3	711	4	AAW36843 Human lac
42	56	93.3	711	4	AAW02341 Human lac
43	56	93.3	711	4	AAW64828 Chronic h
44	56	93.3	711	7	AAE76661 Human lac
45	49	81.7	685	2	AAW11664 Partial p

ALIGNMENTS

RESULT 1
AAW93886
ID AAW93886 standard; peptide; 12 AA.
XX
AC AAW93886;
XX
DT 27-AUG-2003 (revised)
DT 25-JUN-1999 (first entry)
XX
DE Bifidobacterium bifidus stimulating peptide 22.
XX
KW Bifidogenic peptide; protease; treatment; microbe-related disease;
KW bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
KW infection; inflammation; microbial induced tumour; degenerative disorder;
KW diarrhoea; colic; oral microflora; intestinal microflora; caries;
KW vaginal microflora.
XX
OS Bifidobacterium bifidum.
XX
FN W09914231-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-EP005899.
PR 16-SEP-1997; 97DE-01040604.
PR 11-FEB-1998; 98DE-01005385.
XX
PA (FORS/) FORSSMANN W.
XX
PI Forssmann W, Zucht H, Liepke C;
XX
DR WPI; 1999-244022/20.
XX
PT Milk-derived peptides that stimulate Bifidobacterium bifidus.
XX
PS Claim 2; Page 3; 25pp; German.
XX
CC This invention describes milk-derived bifidogenic peptides and their
CC active derivatives or fragments, and combinations of them produced by
CC chemical coupling. Such are produced from bovine or human milk by
CC treatment for 2 hr with proteases, then centrifuging to remove fat and
CC acidifying to pH 2 to precipitate proteins. The solution phase is then
CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
CC Bifidobacterium bifidus and Escherichia coli in presence of the
CC fractions. Those fractions for which (Bw-B0)-(Bw-E0) is at least 0.15 are

CC selected where Bw = germ count after 16 hr culture of B. bifidus in 50%
 CC Elliker broth containing peptide at 0.2 mg/ml, B0 = germ count under
 CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2
 CC mg/ml, B0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W93888 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or carries. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX Sequence 12 AA;
 SQ

Query Match 100.0%; Score 60; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00092;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARRARVYMAVG 12
 Db 1 ARRARVYMAVG 12

RESULT 2
 AAW93878
 ID AAW93878 standard; peptide, 12 AA.
 XX
 AC AAW93878;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-JUN-1999 (first entry)
 XX
 DE Bifidobacterium bifidus stimulating peptide 14.
 XX
 KW Bifidogenic peptide; protease; treatment; microbe-related disease;
 KW bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
 KW infection; inflammation; microbial induced tumour; degenerative disorder;
 KW diarrhoea; colic; oral microflora; intestinal microflora; carries;
 KW vaginal microflora.

XX Bifidobacterium bifidum.
 OS
 PN W09914231-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-EP005899.
 XX
 PR 16-SEP-1997; 97DE-01040604.
 PR 11-FEB-1998; 98DE-01005385.
 XX
 PA (FORS/) FORSSMANN W.
 XX
 PI Forssmann W, Zucht H, Liepke C;
 DR WPI; 1999-244022/20.
 XX
 PT Milk-derived peptides that stimulate Bifidobacterium bifidus.
 XX
 PS Claim 2; Page 3; 25pp; German.

CC This invention describes milk-derived bifidogenic peptides and their
 CC active derivatives or fragments, and combinations of them produced by
 CC chemical coupling. Such are produced from bovine or human milk by
 CC treatment for 2 hr with proteases, then centrifuging to remove fat and
 CC acidifying to pH 2 to precipitate proteins. The solution phase is then
 CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
 CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
 CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
 CC Bifidobacterium bifidus and Escherichia coli in presence of the
 CC fractions. Those fractions for which (Bw-B0)-(Bw-B0) is at least 0.15 are
 CC selected where Bw = germ count after 16 hr culture of B. bifidus in 50%
 CC Elliker broth containing peptide at 0.2 mg/ml, B0 = germ count under

CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2
 CC mg/ml, B0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AAW93865-W93888 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or carries. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX Sequence 12 AA;
 SQ

Query Match 93.3%; Score 56; DB 2; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0045;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARRARVYMAVG 12
 Db 1 ARRARVYMAVG 12

RESULT 3
 AAW93880
 ID AAW93880 standard; peptide, 13 AA.
 XX
 AC AAW93880;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-JUN-1999 (first entry)
 XX
 DE Bifidobacterium bifidus stimulating peptide 16.
 XX
 KW Bifidogenic peptide; protease; treatment; microbe-related disease;
 KW bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
 KW infection; inflammation; microbial induced tumour; degenerative disorder;
 KW diarrhoea; colic; oral microflora; intestinal microflora; carries;
 KW vaginal microflora.

XX Bifidobacterium bifidum.
 OS
 PN W09914231-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-EP005899.
 XX
 PR 16-SEP-1997; 97DE-01040604.
 PR 11-FEB-1998; 98DE-01005385.
 XX
 PA (FORS/) FORSSMANN W.
 XX
 PI Forssmann W, Zucht H, Liepke C;
 DR WPI; 1999-244022/20.
 XX
 PT Milk-derived peptides that stimulate Bifidobacterium bifidus.
 XX
 PS Claim 2; Page 3; 25pp; German.

CC This invention describes milk-derived bifidogenic peptides and their
 CC active derivatives or fragments, and combinations of them produced by
 CC chemical coupling. Such are produced from bovine or human milk by
 CC treatment for 2 hr with proteases, then centrifuging to remove fat and
 CC acidifying to pH 2 to precipitate proteins. The solution phase is then
 CC subjected to reverse-phase high-performance liquid chromatography (HPLC)
 CC and cation-exchange HPLC, the fractions adjusted to salt content below 25
 CC mM (by dialysis or reverse-phase HPLC) and tested for activity by growing
 CC Bifidobacterium bifidus and Escherichia coli in presence of the
 CC fractions. Those fractions for which (Bw-B0)-(Bw-B0) is at least 0.15 are
 CC selected where Bw = germ count after 16 hr culture of B. bifidus in 50%
 CC Elliker broth containing peptide at 0.2 mg/ml, B0 = germ count under
 CC similar conditions in a peptide-free control, Bw = germ count after 16 hr
 CC culture of E. coli in 3 g/l tryptic broth containing peptide at 0.2

CC mg/ml. E0 = germ count under similar conditions in a peptide-free
 CC control. The peptides AA93865-W93868 are used to treat microbe-related
 CC diseases caused by bacteria, fungi, yeast, protozoa, viruses, mycoplasma,
 CC filaria and plasmodia, e.g. infections, inflammation, microbially induced
 CC tumours or degenerative disorders, diarrhoea, colic, abnormalities in
 CC oral, intestinal or vaginal microflora, or carries. (updated on 27-AUG-
 CC 2003 to correct OS field.)
 XX

SQL Sequence 13 AA:

Query Match 93.3%; Score 56; DB 2; Length 13;
 Best Local Similarity 91.7%; Pred. No. 0.0049;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARRAVWMAVG 12
 1 ARRAVWMAVG 12

DB 1 ARRAVWMAVG 12

RESULT 4
 AA971183
 ID AA971183 standard; protein; 687 AA.

XX AA971183;
 XX

DT 27-OCT-1998 (first entry)

DE Mutant human lactoferrin protein designated hLF-5N.
 KM Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
 KM anti-infective; coagulant; complement activation; inhibition;
 KM LPS mediated activation; myelopoiesis; growth promotion;
 KM intestinal epithelial cell; hydroxyl-radical formation;
 KM intestinal iron uptake; excretion.
 XX

OS Synthetic.
 OS Homo sapiens.

XX WO9833509-A2.

XX PD 06-AUG-1998.

XX PF 02-FEB-1998; 98WO-IB000441.

XX PR 03-FEB-1997; 97US-0036859P.

XX PR 02-FEB-1998; 98US-00017043.

XX PA (PHAR-) PHARMING BV.

XX PI Nuijens J, Van Berkel PHC;

XX DR WPI; 1998-437164/37.

PT Compositions containing human lactoferrin and variants - are used for
 PT treating e.g. anaemia, iron-storage disease, inflammation, tumours,
 PT rheumatoid arthritis, ulcerative colitis or infections.
 XX

PS Claim 2; Page; 70pp; English.

XX AA971180-83 represent N-terminally truncated human lactoferrin proteins.
 CC The lactoferrin variants bind heparin with lower affinity than natural
 CC lactoferrin. The lactoferrin variants exhibit biological activities such
 CC as anti-inflammatory, anti-viral and anti-infective activities as well as
 CC a pro- and anti-coagulant effects, modulation of complement activation,
 CC inhibition of LPS mediated activation of neutrophils, inhibition of
 CC myelopoiesis, regulation of transcription, growth promotion of intestinal
 CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
 CC intestinal iron uptake and excretion. Note: this sequence does not appear
 CC in the specification; it was created using information provided
 XX

SQL Sequence 687 AA:

Query Match 93.3%; Score 56; DB 2; Length 687;

Best Local Similarity 91.7%; Pred. No. 0.24;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARRAVWMAVG 12
 1 ARRAVWMAVG 12

DB 336 ARRAVWMAVG 347

RESULT 5
 AA977911

ID AA977911 standard; protein; 687 AA.

XX AA977911;
 XX

DT 22-JAN-2002 (first entry)

DE Human lactoferrin variant hLF-5N.

KM Human; lactoferrin; hLF; infectious disease; inflammatory disease;
 KM excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
 KM anaemia; myelopoiesis; reperfusion injury; cytokine release; proteoglycan;
 KM hLF-5N; mutant; mutein.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX FT Domain 23..26
 XX FT label= Cationic_domain

XX WO200172322-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-NL000253.

XX PR 27-MAR-2000; 2000EP-00201110.

XX PR 27-MAR-2000; 2000US-0193352P.

XX PA (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.

XX PI Van Bree JBM, Nuijens JH;

XX DR WPI; 2001-648424/74.

XX PF Use of lactoferrin for treatment of infectious diseases, inflammatory
 XX diseases and excess of heparin.

XX PS Claim 10; Page; 49pp; English.

XX The sequence represents the human lactoferrin (hLF) protein variant hLF-
 CC 5N. The invention relates to novel methods of treatment using high doses
 CC of lactoferrin. The methods of the invention are useful for the treatment
 CC or prophylaxis of infectious diseases, inflammatory diseases and excess
 CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
 CC anaemia, myelopoiesis, reducing reperfusion injury, cytokine release and
 CC proteoglycan-mediated entry of virus into cells. The advantage of the
 CC method is that the patient is substantially free of side effect responses
 CC to administration of lactoferrin. Therefore large doses of lactoferrin
 CC can be administered. Note: The present sequence is not shown in the
 CC specification but is derived from human wild-type lactoferrin sequence
 CC given in the sequence listing of the specification
 XX

SQL Sequence 687 AA:

Query Match 93.3%; Score 56; DB 4; Length 687;
 Best Local Similarity 91.7%; Pred. No. 0.24;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARRAVWMAVG 12
 1 ARRAVWMAVG 12

DB 336 ARRAVWMAVG 347

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RESULT 6
ID AAW71182 standard; protein; 688 AA.
XX
XX AAW71182;
AC
XX 27-OCT-1998 (first entry)
DT
XX Mutant human lactoferrin protein designated hLF-4N.
DE
XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
KW anti-infective; coagulant; complement activation; inhibition;
KW LPS mediated activation; myeloperoxidase; growth promotion;
KW intestinal epithelial cell; hydroxyl-radical formation;
KW intestinal iron uptake; excretion.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9833509-A2.
PN
XX 06-AUG-1998.
PD
XX 02-FEB-1998; 98WO-IB000441.
PF
XX 03-FEB-1997; 97US-0036859P.
PR
XX 02-FEB-1998; 98US-00017043.
PS
XX (PHAR-) PHARMING BV.
PI
XX Nuijens J, Van Berkel PHC;
DR WPI; 1998-437164/37.
XX
XX Compositions containing human lactoferrin and variants - are used for
PT treating e.g. anaemia, iron-storage disease, inflammation, tumours,
PT rheumatoid arthritis, ulcerative colitis or infections.
XX
XX Claim 2; Page; 70pp; English.
PS
XX AAW71180-83 represent N-terminally truncated human lactoferrin proteins.
CC The lactoferrin variants bind heparin with lower affinity than natural
CC lactoferrin. The lactoferrin variants exhibit biological activities such
CC as anti-inflammatory, anti-viral and anti-infective activities as well as
CC a pro- and anti-coagulant effects, modulation of complement activation,
CC inhibition of LPS mediated activation of neutrophils, inhibition of
CC myeloperoxidase, regulation of transcription, growth promotion of intestinal
CC epithelial cells, inhibition of hydroxyl-radical formation, and a role in
CC intestinal iron uptake and excretion. note: this sequence does not appear
CC in the specification; it was created using information provided
XX
XX Sequence 688 AA;
SQ
Query Match 93.3%; Score 56; DB 2; Length 688;
Best Local Similarity 91.7%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARRARVVMVAAG 12
DB 337 ARRARVVMCAVG 348
RESULT 7
ID AAG77910 standard; protein; 688 AA.
XX
XX AAG77910;
AC
XX 22-JAN-2002 (first entry)
DT
XX Human lactoferrin variant hLF-4N.
DE
XX Human; lactoferrin; hLF; infectious disease; inflammatory disease;
KW

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KW excess of heparin; gastroenteritis; inflammatory bowel disease; sepsis;
KW anaemia; myeloperoxidase; reperfusion injury; cytokine release; proteoglycan;
KW hLF-4N; mutant; mature.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 24..27
FT Domain /label= Cationic_domain
FT
XX
XX WO200172322-A2.
PN
XX 04-OCT-2001.
PD
XX 27-MAR-2001; 2001WO-NI000253.
PF
XX 27-MAR-2000; 2000EP-00201110.
PR
XX 27-MAR-2000; 2000US-0193352P.
PS
XX (PHAR-) PHARMING INTELLECTUAL PROPERTY BV.
PI
XX Van Bree JBMV, Nuijens JH;
DR WPI; 2001-648424/74.
XX
XX Use of lactoferrin for treatment of infectious diseases, inflammatory
PT diseases and excess of heparin.
PT
XX Claim 10; Page; 49pp; English.
PS
XX The sequence represents the human lactoferrin (hLF) protein variant hLF-
CC 4N. The invention relates to novel methods of treatment using high doses
CC of lactoferrin. The methods of the invention are useful for the treatment
CC or prophylaxis of infectious diseases, inflammatory diseases and excess
CC of heparin e.g. gastroenteritis, inflammatory bowel disease, sepsis,
CC anaemia, myeloperoxidase, reducing reperfusion injury, cytokine release and
CC proteoglycan-mediated entry of virus into cells. The advantage of the
CC method is that the patient is substantially free of side effect responses
CC to administration of lactoferrin. Therefore large doses of lactoferrin
CC can be administered. Note: The present sequence is not shown in the
CC specification but is derived from human wild-type lactoferrin sequence
CC given in the sequence listing of the specification
XX
XX Sequence 688 AA;
SQ
Query Match 93.3%; Score 56; DB 4; Length 688;
Best Local Similarity 91.7%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARRARVVMVAAG 12
DB 337 ARRARVVMCAVG 348
RESULT 8
ID AAW71181 standard; protein; 689 AA.
XX
XX AAW71181;
AC
XX 27-OCT-1998 (first entry)
DT
XX Mutant human lactoferrin protein designated hLF-3N.
DE
XX Human; lactoferrin protein; variant; anti-inflammatory; anti-viral;
KW anti-infective; coagulant; complement activation; inhibition;
KW LPS mediated activation; myeloperoxidase; growth promotion;
KW intestinal epithelial cell; hydroxyl-radical formation;
KW intestinal iron uptake; excretion.
XX
XX Synthetic.
OS Homo sapiens.
XX

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